

1	27	100.0	5	2	AAR33009	Aar33009	Alpha-sub
2	27	100.0	5	2	AAR33008	Aar33008	Alpha-sub
3	27	100.0	5	2	AAR33007	Aar33007	Alpha-sub
4	27	100.0	5	2	AAR33010	Aar33010	Alpha-sub
5	27	100.0	5	2	AAR54549	Aar54549	Cholecyst
6	27	100.0	5	2	AAR54551	Aar54551	Cholecyst
7	27	100.0	5	2	AAR54550	Aar54550	Cholecyst
8	27	100.0	5	2	AAR54558	Aar54558	Cholecyst
9	27	100.0	5	2	AAW41587	Aaw41587	Tetrapep
10	27	100.0	5	2	AAW96643	Aaw96643	Substance
11	27	100.0	5	2	AAV50325	Aay50325	Neutroph
12	27	100.0	5	2	AAW92660	Aaw92660	Human tac
13	27	100.0	5	3	AAAB23025	Aab23025	Human/rat
14	27	100.0	5	3	AAV67526	Aay67526	p antago
15	27	100.0	5	4	ABAB91428	Aab91428	Tachykin
16	27	100.0	5	5	ABAB10088	Aab10088	Substance
17	27	100.0	5	5	AAU77845	Aab77845	Tachykin
18	27	100.0	5	7	ADBA94203	Adc94203	High acti
19	27	100.0	5	7	ADFA92530	Adf92530	Substance
20	27	100.0	5	8	ADN95078	Adn95078	Mammaliar
21	27	100.0	5	8	ADRA43771	Adt43771	Human mac
22	27	100.0	5	9	ADVA44808	Adt44808	Mammaliar
23	27	100.0	6	1	AAAP40519	Aap40519	Sequence
24	27	100.0	6	1	AAAP50694	Aap50694	Sequence

25	27	100.0	6	1	AAp50632	AAp50632	Substance
26	27	100.0	6	1	AAp61486	AAp61486	Peptide h
26	27	100.0	6	2	AAp07893	AAp07893	Clyclopept
28	27	100.0	6	2	AAp21959	AAp21959	Substance
28	27	100.0	6	2	AAp21694	AAp21694	Cyclic ta
29	27	100.0	6	2	AAp96866	AAp96866	Substance
30	27	100.0	6	2	AAp92706	AAp92706	Human tac
31	27	100.0	6	2	AAp92659	AAp92659	Human tac
32	27	100.0	6	2	AAp92659	AAp92659	Human tac
32	27	100.0	6	3	AAp67575	AAp67575	p antagonist
33	27	100.0	6	3	AAp67575	AAp67575	p antagonist
34	27	100.0	6	4	AAp82436	AAp82436	Fluorinat
35	27	100.0	6	4	AAp82436	AAp82436	Fluorinat
35	27	100.0	6	4	AAp91421	AAp91421	Tachykini
36	27	100.0	6	4	AAp91425	AAp91425	Tachykini
37	27	100.0	6	4	AAp91419	AAp91419	techykini
38	27	100.0	6	4	AAp99351	AAp99351	Atypical
39	27	100.0	6	4	AAp98884	AAp98884	Chimeric
40	27	100.0	6	4	AAp98886	AAp98886	Chimeric
41	27	100.0	6	4	AAp10086	AAp10086	Substance
42	27	100.0	6	5	AAp94202	AAp94202	High acitv
43	27	100.0	6	7	AAp21956	AAp21956	Substance
44	27	100.0	7	2	AAp21957	AAp21957	Substance
45	27	100.0	7	2	AAp21957	AAp21957	Substance

ALIGNMENTS

RESULT 1	
AAAR33009	
ID	AAAR33009 standard; peptide; 5 AA.
XX	
AC	AAAR33009;
XX	
DT	25-MAR-2003 (revised)
DT	02-APR-1993 (first entry)
XX	
DE	Alpha-substituted short peptide.
XX	
KW	CKK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
KW	Improved bioavailability.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site 4 Location/Qualifiers
FT	/note= "alpha-Me-Leu"
FT	Modified-site 5
FT	/note= "Met-NH2"
XX	
PN	WO9219254-A1.
XX	
PD	12-NOV-1992.
XX	
PF	15-APR-1992; 92WO-US003119.
XX	
PR	24-APR-1991; 91US-00690755.
PR	20-MAR-1992; 92US-00852086.
XX	
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Howeell DC, Hughes J, Richardson RS, Howson W;
XX	
DR	WPI; 1992-398522/48.
XX	
PT	New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT	depression, cancer, asthma, psychosis, arthritis, etc.
XX	
PS	Claim 3; Page 41; 46pp; English.
XX	
CC	The peptide is a specifically claimed example of a group of generically
CC	claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC	substituent on an alpha-C atom in the chain. Such substitution may modify
CC	the bioavailability, stability or absorbability of the peptide and hence

CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5
Db 1 FFGLM 5

RESULT 2
AAR33008

ID AAR33008 standard; peptide; 5 AA.

AC AAR33008;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

DE Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX improved bioavailability.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 2 /note= "alpha-Me-Phe"

FT Modified-site 5 /note= "Met-NH2"

PN WO9219254-A1.

PD 12-NOV-1992.

PF 15-APR-1992; 92WO-US003119.

PR 24-APR-1991; 91US-00690755.

PR 20-MAR-1992; 92US-00852086.

PA (WARN) WARNER LAMBERT CO.

PI Horwell DC, Hughes J, Richardson RS, Howson W;

DR WPI; 1992-398522/48.

PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

CC The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify
CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,

CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5
Db 1 FFGLM 5

RESULT 3
AAR33007

ID AAR33007 standard; peptide; 5 AA.

AC AAR33007;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

DE Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX improved bioavailability.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1 /note= "alpha-Me-Phe"

FT Modified-site 5 /note= "Met-NH2"

PN WO9219254-A1.

PD 12-NOV-1992.

PF 15-APR-1992; 92WO-US003119.

PR 24-APR-1991; 91US-00690755.

PR 20-MAR-1992; 92US-00852086.

PA (WARN) WARNER LAMBERT CO.

PI Horwell DC, Hughes J, Richardson RS, Howson W;

DR WPI; 1992-398522/48.

PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

CC The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify
CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:18:04 ; Search time 20 Seconds

(without alignments)
24.054 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 FFGIM 5

Scoring table: BIOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1 A60654	substance P - guin
2	27	100.0	11	1 SPHO	substance P - hors
3	27	100.0	11	1 JN0023	substance P - chic
4	27	100.0	11	2 S33300	probable substance
5	27	100.0	11	2 B60409	substance P-like P
6	27	100.0	11	2 F60409	substance P-like P
7	27	100.0	11	2 S23308	substance P - like P
8	24	88.9	10	2 B49581	substance P - rain
9	24	88.9	10	2 B61033	ranatokinin II - ye
10	24	88.9	10	2 A49581	ranatokinin B -
11	24	88.9	10	2 A24867	salokinin I - yel
12	24	88.9	10	2 S07203	scyllorhizin I - s
13	24	88.9	11	2 S07201	uroolein - frog (
14	24	88.9	11	2 A61033	physalaemin - frog
15	22	81.5	12	2 A61033	ranatokinin A -
16	22	81.5	12	2 T06925	tachykinin - Afri
17	22	77.8	10	2 S07202	hypothetical prote
18	21	77.8	10	2 G61033	phyllomedulin - tw
19	21	77.8	10	2 S27178	ranatokinin C -
20	21	77.8	11	1 E00C	neurokinin A-relat
21	21	77.8	11	1 E00C	eledotisin - musky
22	21	77.8	11	1 E00C	eledotisin - curled
23	21	77.8	19	2 S60332	substance P - Atla
24	21	77.8	24	2 S15649	phospholipase A2 (
25	20	74.1	10	1 SPPGNK	H-transferring tw
26	20	74.1	10	2 JN0024	neurokinin K - pig
27	20	74.1	10	2 S23307	neurokinin A - chi
28	20	74.1	10	2 S23186	neurokinin A - rai
29	20	74.1	11	2 C60409	neurokinin A - Atl
30	20	74.1	11	2 C60409	kassinin-like pept

30	20	74.1	11	2 B60409	kassinin-like pept
31	20	74.1	11	2 D60409	kassinin-like pept
32	20	74.1	12	2 S10059	tachykinin - Afri
33	20	74.1	12	2 S07206	kassinin - Senegal
34	20	74.1	16	2 A60839	neurokinin A homol
35	20	74.1	18	2 B24867	scyllorhizin II -
36	20	74.1	21	2 JH0361	carassin - goldfis
37	19	70.4	12	2 S74144	aggrasin - bovine
38	19	70.4	18	2 I52551	brain-derived neur
39	18	66.7	5	2 FT0278	Ig heavy chain CRD
40	18	66.7	10	2 PH0807	T-cell receptor al
41	18	66.7	12	2 S26556	T-cell receptor be
42	18	66.7	12	2 S26554	T-cell receptor be
43	18	66.7	12	2 S26559	T-cell receptor be
44	18	66.7	12	2 S26555	T-cell receptor be
45	18	66.7	12	2 PH1467	T-cell receptor be

ALIGNMENTS

```
RESULT 1
A60654
substance P - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: A60654
R/Murphy, R.
Neuropeptides 14, 105-110, 1989
A/Title: Primary amino acid sequence of guinea-pig substance P.
A/Reference number: A60654; PMID:90044685; PMID:2478925
A/Accession: A60654
A/Molecule type: protein
A/Residues: 1-11 <MUR>
A/Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
F/1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match      100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 FFGIM 5
DB      7 FFGIM 11

RESULT 2
SPHO
substance P - horse
C/Species: Equus caballus (domestic horse)
C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C/Accession: A01558
R/Studer, R.O.; Trzeciak, A.; Lergier, W.
Hely. Chim. Acta 56, 860-866, 1973
A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarms.
A/Reference number: A01558
A/Accession: A01558
A/Molecule type: protein
A/Residues: 1-11 <STU>
A/Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; hormone
F/1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match      100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 FFGIM 5
DB      7 FFGIM 11
```

RESULT 3

JN0023

Substance P - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: JN0023

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263; PMID:2452461

A:Accession: JN0023

A:Molecule type: protein

A:Residues: 1-11 <CON>

A:Cross-references: UNIPROT:P19850; UNIPARC:UPI0000035243

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

DB 7 FFGLM 11

RESULT 4

S33300

Probable substance P - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S33300

R:Maugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A:Title: Primary structures and biological activities of substance-P-related peptides for

A:Reference number: S33300; MUID:93292508; PMID:7685693

A:Accession: S33300

A:Molecule type: protein

A:Residues: 1-11 <MAU>

A:Cross-references: UNIPROT:P41333; UNIPARC:UPI0000136FDB

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

DB 7 FFGLM 11

RESULT 5

E60409

Substance P-like peptide I - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: E60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: E60409

A:Molecule type: protein

A:Residues: 1-11 <STM>

A:Cross-references: UNIPROT:P42989; UNIPARC:UPI0000136FDB

C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

DB 7 FFGLM 11

RESULT 6

F60409

Substance P-like peptide II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: F60409

R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: F60409

A:Molecule type: protein

A:Residues: 1-11 <STM>

A:Cross-references: UNIPROT:P42990; UNIPARC:UPI0000136FDB

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

DB 7 FFGLM 11

RESULT 7

S23308

Substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004

C:Accession: S23308

R:Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod

A:Reference number: S23186; MUID:92298992; PMID:1376687

A:Accession: S23308

A:Molecule type: protein

A:Residues: 1-11 <JEN>

A:Cross-references: UNIPROT:P28499; UNIPARC:UPI0000035254

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas-

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

DB 7 FFGLM 11

RESULT 8

B9581

Salokinin II - yellow fever mosquito

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:17:04 ; Search time 122.5 Seconds
(without alignments)
28.797 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 34439

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UnIProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	11	TKN4_PSEGU	P42989 pseudophryn
2	27	100.0	11	TKN5_PSEGU	P42990 pseudophryn
3	27	100.0	11	TKNA_CAVPO	P67932 cavia porce
4	27	100.0	11	TKNA_CHICK	P19850 gallus gall
5	27	100.0	11	TKNA_HORSE	P67933 equus caball
6	27	100.0	11	TKNA_ONCMY	P28499 oncorhynch
7	27	100.0	11	TKNA_SCYCA	P41333 scyllorhinu
8	24	88.9	10	TKN1_SCYCA	P08608 scyllorhinu
9	24	88.9	10	TKNB_RANCA	P22689 rana catesb
10	24	88.9	10	TKS1_AEDAE	P42634 aedes aegypt
11	24	88.9	10	TKS2_AEDAE	P42635 aedes aegypt
12	24	88.9	11	TKN1_UPEIN	P82026 uperoleia i
13	24	88.9	11	TKN1_UPERU	P08612 uperoleia i
14	24	88.9	11	TKN2_UPERU	P08616 uperoleia r
15	24	88.9	11	TKNA_RANCA	P22688 rana catesb
16	24	88.9	11	TKNA_RANRI	P29207 rana ridibu
17	24	88.9	11	TKN1_PHYPU	P08615 physalaemus
18	24	88.9	11	OJUAR8_AEDAE	OJ9488 aedes aegypt
19	24	88.9	14	TKNM_RANNA	P40951 rana margar
20	24	88.9	25	O80VX3_MOUSE	O80VX3 mus musculu
21	24	88.9	26	O4TDP2_TETNG	O4Tdf2 tetradon n
22	23	85.2	30	Q5N289_STNPF	Q5N289 synecococc
23	22	81.5	12	TKN2_KASMA	P08614 kassina mac
24	22	81.5	25	O8K1T2_MOUSE	O8K1T2 mus musculu
25	22	81.5	27	O4YTJ2_PLABE	O4YTJ2 plasmodium
26	22	81.5	28	PTKL_CVAPA	P48102 cyamophora
27	21	77.8	10	TKNB_RANRI	P29135 rana ridibu
28	21	77.8	10	TKNC_RANCA	P22690 rana catesb
29	21	77.8	10	TKN1_PHYPU	P08610 phyllomedus
30	21	77.8	10	O76ML8_PTELE	O76ML8 eurypharynx
31	21	77.8	11	TKNA_GADMO	P28498 gadus morhu

32	21	77.8	11	TKN ELECT	P62933 eleidone cir
33	21	77.8	11	TKN ELEMO	P62934 eleidone mos
34	21	77.8	19	P425_HUMAN	P24606 homo sapien
35	21	77.8	19	O9S8E2_SPIOL	O9S8E2 spinnacia ol
36	21	77.8	23	O99221_MELTA	O99221 meloidogyne
37	21	77.8	23	O4XB06_PLACH	O4XB06 plasmodium
38	21	77.8	27	O4SBA4_TETNG	O4SBA4 tetradon n
39	21	77.8	29	O673E3_SCHLR	O673E3 dehalococc
40	20	74.1	10	TKNB_CHICK	P19851 gallus gall
41	20	74.1	10	TKNB_GADMO	P69144 gadus morhu
42	20	74.1	10	TKNB_ONCMY	P69143 oncorhynch
43	20	74.1	10	TKNK_PIG	P67934 sus scrofa
44	20	74.1	10	TKNK_RANRI	P67935 rana ridibu
45	20	74.1	10	TRP6_LEUMA	P81738 leucophaea

ALIGNMENTS

RESULT 1

ID	TKN4_PSEGU	STANDARD	PRT	11 AA.
AC	P42989;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Substance P-like peptide I (PG-SPI)			
OS	Pseudophryne guentheri (Guenther's toadlet).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;			
OC	Myobatrachinae; Pseudophryne.			
OX	NCBI_TaxID=30349;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RC	TISSUE=Skin secretion;			
RA	MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;			
RA	Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,			
RA	Roberts J.D., Melchiorri P., Erppamer V.,			
RT	"Six novel tachykinin- and bombesin-related peptides from the skin of			
RT	the Australian frog Pseudophryne guentheri.";			
RL	Peptides 11:299-304 (1990).			
CC	-1- FUNCTION: Tachykinins are active peptides which excite neurons,			
CC	evoked behavioral responses, are potent vasodilators and			
CC	secretagogues, and contract (directly or indirectly) many smooth			
CC	muscles.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the skin glands.			
CC	-1- SIMILARITY: Belongs to the tachykinin family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
DR	PIR: B60409; E60409.			
DR	InterPro: IPR002040; Tachy Neurokinin.			
DR	InterPro: IPR008215; Tachykinin.			
DR	Pfam: PF02202; Tachykinin; 1.			
DR	SMART: SM00203; TK; 1.			
DR	PROSITE: PS00267; TACHYKININ; 1.			
KW	Amidation; Amphibian defense peptide; Direct protein sequencing;			
KW	Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.			
FT	MOD_RSS 1 1 Pyrrolidone carboxylic acid.			
FT	MOD_RSS 1 1 Methionine amide.			
SQ	SEQUENCE 11 AA; 1294 MW; 3A247CC9CB1AB7 CRC64;			
QY	Query Match 100.0%; Score 27; DB 1; Length 11;			
	Best Local Similarity 100.0%; Pred. No. 32;			
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
	1 FFGIM 5			

Db 7 FFGLM 11

RESULT 2

TKNS_PSEGU STANDARD; PRT; 11 AA.

AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Substance P-like peptide II (PG-SP11).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;

OC Myobatrachine; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;

RA Sirmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberto J.D., Melchiorri P., Brismar V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykynins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: F60409; F60409.

CC InterPro: IPR002040; Tachy_Neurokinin.

CC Pfam: PF02202; Tachykinin; 1.

CC PROSITE: PS00267; TACHYKININ; 1.

CC DR Annotation: Amphibian defense peptide; Direct protein sequencing;

CC KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.

CC MOD_RES 1 1 Pyrrolidone carboxylic acid.

CC FT MOD_RES 11 11 Methionine amide.

CC FT SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

CC SQ

Query Match 100.0%; Score 27; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FFGLM 5

Db 7 FFGLM 11

RESULT 3

TKNA_CAVPO STANDARD; PRT; 11 AA.

AC P67932; P01290;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Substance P.

GN Name=TAC1; Synonyms=NKA, NKNA, TAC2;

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

OC Hystriognathia; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Small intestine;

RX MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8;

RA Murphy R.;

RT "Primary amino acid sequence of guinea-pig substance P.";

RL Neuropeptides 14:105-110(1989).

CC -1- FUNCTION: Tachykynins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: A60654; A60654.

CC InterPro: IPR002040; Tachy_Neurokinin.

CC Pfam: PF02202; Tachykinin; 1.

CC PROSITE: PS00267; TACHYKININ; 1.

CC DR Annotation: Direct protein sequencing; Neuropeptide; Neurotransmitter;

CC KW Tachykinin.

CC MOD_RES 11 11 Methionine amide.

CC FT SEQUENCE 11 AA; 1349 MW; 3E757F83C9D6C67 CRC64;

CC SQ

Query Match 100.0%; Score 27; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FFGLM 5

Db 7 FFGLM 11

RESULT 4

TKNA_CHICK STANDARD; PRT; 11 AA.

AC P19850;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Substance P.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;

RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;

RT "[Arg3]substance P and neurokinin A from chicken small intestine.";

RL Regul. Pept. 20:171-180(1988).

CC -1- FUNCTION: Tachykynins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: JN0023; JN0023.

CC InterPro: IPR002040; Tachy_Neurokinin.

CC Pfam: PF02202; Tachykinin; 1.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:06:43 ; Search time 20 Seconds
(without alignments)
20.669 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	5	1 US-07-934-553-2	Sequence 2, Appli
2	27	100.0	5	1 US-08-225-474-2	Sequence 2, Appli
3	27	100.0	5	1 US-07-737-371E-6	Sequence 6, Appli
4	27	100.0	5	2 US-09-265-690C-1	Sequence 1, Appli
5	27	100.0	5	2 US-09-623-548A-604	Sequence 604, App
6	27	100.0	5	2 US-10-134-187-3	Sequence 3, Appli
7	27	100.0	5	1 US-09-657-276-604	Sequence 604, App
8	27	100.0	6	1 US-07-934-553-3	Sequence 3, Appli
9	27	100.0	6	1 US-08-225-474-3	Sequence 3, Appli
10	27	100.0	6	1 US-08-430-238-15	Sequence 15, Appli
11	27	100.0	6	1 US-07-737-371E-5	Sequence 5, Appli
12	27	100.0	6	2 US-09-317-125-5	Sequence 5, Appli
13	27	100.0	6	2 US-09-428-692-39	Sequence 39, Appli
14	27	100.0	6	2 US-09-428-692-41	Sequence 41, Appli
15	27	100.0	6	2 US-09-623-548A-595	Sequence 595, App
16	27	100.0	6	2 US-09-623-548A-597	Sequence 597, App
17	27	100.0	6	2 US-09-623-548A-601	Sequence 601, App
18	27	100.0	6	2 US-09-657-276-595	Sequence 595, App
19	27	100.0	6	2 US-09-657-276-597	Sequence 597, App
20	27	100.0	6	2 US-09-657-276-601	Sequence 601, App
21	27	100.0	7	1 US-07-712-828B-7	Sequence 7, Appli
22	27	100.0	7	1 US-07-737-371E-8	Sequence 8, Appli
23	27	100.0	7	2 US-09-428-692-42	Sequence 42, Appli
24	27	100.0	7	2 US-09-623-548A-596	Sequence 596, App
25	27	100.0	7	2 US-09-623-548A-607	Sequence 607, App
26	27	100.0	7	2 US-10-134-187-2	Sequence 2, Appli
27	27	100.0	7	2 US-09-657-276-596	Sequence 596, App

28	27	100.0	7	2 US-09-657-276-607	Sequence 607, App
29	27	100.0	8	1 US-07-737-371E-10	Sequence 10, Appli
30	27	100.0	8	1 US-07-737-371E-56	Sequence 56, Appli
31	27	100.0	8	2 US-09-623-548A-583	Sequence 583, App
32	27	100.0	8	2 US-09-623-548A-592	Sequence 592, App
33	27	100.0	8	2 US-09-623-548A-600	Sequence 600, App
34	27	100.0	8	2 US-09-657-276-583	Sequence 583, App
35	27	100.0	8	2 US-09-657-276-592	Sequence 592, App
36	27	100.0	8	2 US-09-657-276-600	Sequence 600, App
37	27	100.0	9	1 US-07-737-371E-60	Sequence 60, Appli
38	27	100.0	9	2 US-09-623-548A-545	Sequence 545, App
39	27	100.0	9	2 US-09-623-548A-622	Sequence 622, App
40	27	100.0	9	2 US-10-134-187-1	Sequence 1, Appli
41	27	100.0	9	2 US-09-657-276-545	Sequence 545, App
42	27	100.0	9	2 US-09-657-276-622	Sequence 622, App
43	27	100.0	10	1 US-08-088-322-6	Sequence 6, Appli
44	27	100.0	10	1 US-08-437-820-6	Sequence 6, Appli
45	27	100.0	10	1 US-07-737-371E-9	Sequence 9, Appli

ALIGNMENTS

```
RESULT 1
US-07-934-553-2
; Sequence 2, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGB
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGWIS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-90333CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-934-553-2

Query Match      100.0%; Score 27; DB 1; Length 5;
Best local similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 FFGIM 5
      |||||
```

Db 1 FFGLM 5

RESULT 2

US-08-225-474-2

Sequence 2, Application US/08225474

Patent No. 5560915

GENERAL INFORMATION:

APPLICANT: Patterson, Roy

TITLE OF INVENTION: Method and Composition for Treating

TITLE OF INVENTION: 198 Mediated Allergies

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut

STREET: 100 S. Wacker Drive, Suite 960

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-4002

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/225,474

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,553

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/705,071

FILING DATE: 24-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Tilton, Timothy L.

REGISTRATION NUMBER: 16, 926

REFERENCE/DOCKET NUMBER: NU 9033-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)-456-8000

TELEFAX: (312)-456-7776

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-225-474-2

Query Match 100.0%; Score 27; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

Db 1 FFGLM 5

RESULT 3

US-07-737-371E-6

Sequence 6, Application US/07737371E

Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E

FILING DATE: 29-JUL-1991

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/559,172

FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00108/028002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-737-371E-6

Query Match 100.0%; Score 27; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

Db 1 FFGLM 5

RESULT 4

US-09-265-690C-1

Sequence 1, Application US/09265690C

Patent No. 6372440

GENERAL INFORMATION:

APPLICANT: Wells, Ibert

TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma

FILE REFERENCE: 1427001

CURRENT APPLICATION NUMBER: US/09/265,690C

CURRENT FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 5

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (5)..(5)

OTHER INFORMATION: AMIDATION

US-09-265-690C-1

Query Match 100.0%; Score 27; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5

Db 1 FFGLM 5

RESULT 5

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:13:24 ; Search time 57.5 Seconds

(without alignments)
36.333 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 PFGLM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_MA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	3	US-09-265-690C-1
2	27	100.0	5	4	US-10-053-669-1
3	27	100.0	5	4	US-10-134-187-3
4	27	100.0	5	4	US-10-688-741-3
5	27	100.0	5	4	US-10-805-881-1
6	27	100.0	5	5	US-10-720-039-3
7	27	100.0	5	5	US-10-497-628-15
8	27	100.0	5	6	US-11-066-697-604
9	27	100.0	5	6	US-11-025-494-3
10	27	100.0	6	4	US-10-168-789A-38
11	27	100.0	6	5	US-10-497-628-14
12	27	100.0	6	6	US-11-066-697-595
13	27	100.0	6	6	US-11-066-697-597
14	27	100.0	6	6	US-11-066-697-601
15	27	100.0	7	4	US-10-036-542-110
16	27	100.0	7	4	US-10-036-542-111
17	27	100.0	7	4	US-10-168-789A-37
18	27	100.0	7	4	US-10-134-187-2
19	27	100.0	7	4	US-10-688-741-2
20	27	100.0	7	5	US-10-720-039-2
21	27	100.0	7	5	US-10-497-628-13
22	27	100.0	7	6	US-11-066-697-596
23	27	100.0	7	6	US-11-066-697-607
24	27	100.0	7	6	US-11-025-494-2
25	27	100.0	8	4	US-10-168-789A-36
26	27	100.0	8	5	US-10-497-628-12
27	27	100.0	8	6	US-11-066-697-583

28	27	100.0	8	6	US-11-066-697-592	Sequence 592, App
29	27	100.0	8	6	US-11-066-697-600	Sequence 600, App
30	27	100.0	9	4	US-10-036-542-112	Sequence 112, App
31	27	100.0	9	4	US-10-168-789A-35	Sequence 35, App
32	27	100.0	9	4	US-10-134-187-1	Sequence 1, Appli
33	27	100.0	9	4	US-10-688-741-1	Sequence 1, Appli
34	27	100.0	9	5	US-10-720-039-1	Sequence 1, Appli
35	27	100.0	9	6	US-11-066-697-545	Sequence 545, App
36	27	100.0	9	6	US-11-066-697-622	Sequence 622, App
37	27	100.0	9	6	US-11-025-494-1	Sequence 1, Appli
38	27	100.0	10	4	US-10-168-789A-34	Sequence 34, Appli
39	27	100.0	10	5	US-10-451-304-1	Sequence 1, Appli
40	27	100.0	10	6	US-11-066-697-621	Sequence 621, App
41	27	100.0	10	6	US-11-079-147-71	Sequence 71, Appli
42	27	100.0	11	3	US-09-265-690C-3	Sequence 3, Appli
43	27	100.0	11	3	US-09-935-682-64	Sequence 64, Appli
44	27	100.0	11	3	US-09-841-091B-26	Sequence 26, Appli
45	27	100.0	11	3	US-09-988-792-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
; Sequence 1, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mo.
; FILE REFERENCE: 1427001
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

Query Match      100.0%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PFGLM 5
Db      1 PFGLM 5

RESULT 2
US-10-053-669-1
; Sequence 1, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
```

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5) (5)
OTHER INFORMATION: AMIDATION
US-10-033-669-1

Query Match 100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
Db 1 FFGLM 5

RESULT 3
US-10-134-187-3
Sequence 3, Application US/10134187
Publication No. US20030202981A1
GENERAL INFORMATION:
APPLICANT: Kream, Richard M.
APPLICANT: Kream, Richard M.
TITLE OF INVENTION: Chimeric Hybrid Analgesics
FILE REFERENCE: Kream
CURRENT APPLICATION NUMBER: US/10/134,187
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: mammalian
US-10-134-187-3

Query Match 100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
Db 1 FFGLM 5

RESULT 4
US-10-688-741-3
Sequence 3, Application US/10688741
Publication No. US20040106636A1
GENERAL INFORMATION:
APPLICANT: Kream, Richard M.
APPLICANT: Kream, Richard M.
TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
FILE REFERENCE: Kream
CURRENT APPLICATION NUMBER: US/10/688,741
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: mammalian
US-10-688-741-3

Query Match 100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
Db 1 FFGLM 5

RESULT 5
US-10-805-881-1
Sequence 1, Application US/10805881
Publication No. US20040171093A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert C.
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
FILE REFERENCE: 800812-0005
CURRENT APPLICATION NUMBER: US/10/805,881
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 10/053,669
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 10/695,536
PRIOR FILING DATE: 2003-10-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5) (5)
OTHER INFORMATION: AMIDATION
US-10-805-881-1

Query Match 100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
Db 1 FFGLM 5

RESULT 6
US-10-720-039-3
Sequence 3, Application US/10720039
Publication No. US20040259786A1
GENERAL INFORMATION:
APPLICANT: Kream, Richard M.
APPLICANT: Kream, Richard M.
TITLE OF INVENTION: Method Of Transporting A Chimeric Hybrid Molecule Across The Bloo
FILE REFERENCE: Kream
CURRENT APPLICATION NUMBER: US/10/720,039
CURRENT FILING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: mammalian
US-10-720-039-3

Query Match 100.0%; Score 27; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
Db 1 FFGLM 5

RESULT 7
US-10-497-628-15
Sequence 15, Application US/10497628
Publication No. US20050009752A1
GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:09:53 ; Search time 3.57143 Seconds
(without alignments)
4.243 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 PFGIM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 7285

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	81.5	19	US-10-503-575-149	Sequence 149, App
2	19	70.4	19	US-11-054-515-2170	Sequence 2170, App
3	19	70.4	21	US-10-939-890-552	Sequence 552, App
4	18	66.7	11	US-11-054-515-3165	Sequence 3165, App
5	18	66.7	13	US-10-511-559-1043	Sequence 1043, App
6	18	66.7	13	US-10-511-559-1044	Sequence 1044, App
7	18	66.7	13	US-10-511-559-1045	Sequence 1045, App
8	18	66.7	13	US-10-511-559-1046	Sequence 1046, App
9	18	66.7	13	US-10-511-559-1047	Sequence 1047, App
10	18	66.7	13	US-10-511-559-1048	Sequence 1048, App
11	18	66.7	14	US-10-986-501-322	Sequence 322, App
12	18	66.7	19	US-11-038-501-13	Sequence 13, App1
13	18	66.7	19	US-11-059-633-16	Sequence 16, App1
14	18	66.7	21	US-10-939-890-509	Sequence 509, App
15	18	66.7	21	US-10-939-890-517	Sequence 517, App
16	18	66.7	21	US-10-939-890-574	Sequence 574, App
17	17	63.0	8	US-11-054-515-1098	Sequence 3098, App
18	17	63.0	12	US-11-054-515-2884	Sequence 2884, App
19	17	63.0	15	US-11-054-515-2976	Sequence 2976, App
20	17	63.0	16	US-11-054-515-3071	Sequence 3071, App
21	17	63.0	17	US-11-054-515-3025	Sequence 3025, App
22	17	63.0	18	US-11-054-515-2752	Sequence 2752, App
23	17	63.0	18	US-11-054-515-2802	Sequence 2802, App
24	17	63.0	20	US-11-054-515-2131	Sequence 2131, App
25	16	59.3	8	US-11-044-051-80	Sequence 80, App1

26	16	59.3	9	7	US-11-044-051-78	Sequence 78, App1
27	16	59.3	9	7	US-11-044-051-79	Sequence 79, App1
28	16	59.3	10	7	US-11-044-051-77	Sequence 77, App1
29	16	59.3	10	7	US-11-044-051-85	Sequence 85, App1
30	16	59.3	10	7	US-11-044-051-87	Sequence 87, App1
31	16	59.3	10	7	US-11-044-051-88	Sequence 88, App1
32	16	59.3	13	1	US-10-986-501-161	Sequence 161, App
33	16	59.3	13	1	US-10-986-501-192	Sequence 192, App
34	16	59.3	16	7	US-11-044-051-81	Sequence 81, App1
35	16	59.3	16	7	US-11-054-515-2883	Sequence 2883, App
36	16	59.3	16	7	US-11-054-515-2893	Sequence 2893, App
37	16	59.3	19	1	US-10-503-575-161	Sequence 161, App
38	16	59.3	20	7	US-11-022-562-125	Sequence 125, App
39	16	59.3	21	7	US-11-054-515-2865	Sequence 2865, App
40	15	55.6	8	7	US-11-054-515-3132	Sequence 3132, App
41	15	55.6	12	1	US-10-923-605-4	Sequence 4, App1
42	15	55.6	12	1	US-10-934-818-4	Sequence 4, App1
43	15	55.6	13	1	US-10-511-559-478	Sequence 478, App
44	15	55.6	13	1	US-10-511-559-479	Sequence 479, App
45	15	55.6	13	1	US-10-511-559-480	Sequence 480, App

ALIGNMENTS

```
RESULT 1
US-10-503-575-149
Sequence 149, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Drifheut, Jan Wouter
APPLICANT: Van Veele, Petrus Antonius
APPLICANT: Koning, Frits
TITLE OF INVENTION: NOVEL BIOTYPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
FILE REFERENCE: 2799/72843-PCT-US
CURRENT APPLICATION NUMBER: US/10/503,575
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: PCT/NL03/00077
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: EP 02075456.0
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 149
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-149

Query Match      81.5%: Score 22; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 PFGIM 4
Db      12 PFGIM 15

RESULT 2
US-11-054-515-2170
Sequence 2170, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
```

```

; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2170
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2170
```

```

Query Match          70.4%; Score 19; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FFG 4
        |||
Db      11 YFGL 14
```

RESULT 3

```
US-10-939-890-552
; Sequence 552, Application US/10939890
; Publication No. US20050250700A1
```

GENERAL INFORMATION:

```

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buesat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palanappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
```

```

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
```

```

; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
```

```

; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
```

```

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
```

```

; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
```

```

; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
```

```

; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
```

```

; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 552
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-552
```

```

Query Match          70.4%; Score 19; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 FFG 5
        |||
Db      10 FFGCM 14
```

RESULT 4

```
US-11-054-515-3165
; Sequence 3165, Application US/11054515
; Publication No. US20050255532A1
```

GENERAL INFORMATION:

```

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P0923P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3165
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3165
```

```

Query Match          66.7%; Score 18; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FFG 3
        |||
Db      2 FFG 4
```

RESULT 5

```
US-10-511-559-1043
```

```

; Sequence 1043, Application US/10511559
; Publication No. US20050256304A1
```

GENERAL INFORMATION:

```

; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 01:57:32 ; Search time 182 Seconds
(without alignments)
12.071 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 56929

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	5	2	AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2	AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2	AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2	AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2	AAR54549	Aar54549 Cholecyst
6	27	100.0	5	2	AAR54551	Aar54551 Cholecyst
7	27	100.0	5	2	AAR54550	Aar54550 Cholecyst
8	27	100.0	5	2	AAR54548	Aar54548 Cholecyst
9	27	100.0	5	2	AAW41687	AAW41687 Tetrapt
10	27	100.0	5	2	AAW99643	AAW99643 Substance
11	27	100.0	5	2	AAV50325	AAV50325 Neutrophil
12	27	100.0	5	2	AAW92660	AAW92660 Human tac
13	27	100.0	5	3	AAW23025	AAW23025 Human/rat
14	27	100.0	5	3	AAV67576	AAV67576 P antagon
15	27	100.0	5	4	AAV91428	AAV91428 Tachykini
16	27	100.0	5	5	ABBI10088	ABBI10088 Substance
17	27	100.0	5	5	AAU77845	AAU77845 Tachykini
18	27	100.0	5	7	ADBE94203	ADBE94203 High acti
19	27	100.0	5	7	ADP92530	ADP92530 Substance
20	27	100.0	5	8	ADN95078	ADN95078 Mammalian
21	27	100.0	5	8	ADR43771	ADR43771 Human mag
22	27	100.0	5	9	ADV44808	ADV44808 Mammalian
23	24	88.9	5	2	AAW92702	AAW92702 Human tac
24	24	88.9	5	5	ABBI10089	ABBI10089 Substance

25	24	88.9	5	7	ADBE94204	ADBE94204 High acti
26	22	81.5	4	9	ADY04142	ADY04142 Peptide d
27	22	81.5	5	2	AAR27697	Aar27697 Cyclic ta
28	22	81.5	5	2	AAW92703	AAW92703 Human tac
29	22	81.5	5	2	AAW92701	AAW92701 Human tac
30	21	77.8	4	2	AAW41683	AAW41683 Peptide u
31	21	77.8	4	3	AAV31075	AAV31075 Non-cross
32	21	77.8	4	3	AAW33026	AAW33026 Human/rat
33	21	77.8	4	3	AAV67577	AAV67577 P antagon
34	21	77.8	4	4	AAW91447	AAW91447 Tachykini
35	21	77.8	4	5	ABBI10091	ABBI10091 Substance
36	21	77.8	4	5	AAU77846	AAU77846 Tachykini
37	21	77.8	4	7	ADBE94198	ADBE94198 High acti
38	21	77.8	4	8	ADR43772	ADR43772 Human mag
39	21	77.8	5	4	AAW91389	AAW91389 Tachykini
40	21	77.8	5	5	ABBI10090	ABBI10090 Substance
41	21	77.8	5	6	AAE35975	AAE35975 Zea may
42	21	77.8	5	7	ADBE94205	ADBE94205 High acti
43	21	77.8	5	8	ADRO3603	ADRO3603 E. coli m
44	20	74.1	5	2	AAW80134	AAW80134 COOH-term
45	20	74.1	5	2	AAW41695	Aar41695 GHRP-6 (G

ALIGNMENTS

RESULT 1		
AAW33009	AAW33009 standard; peptide; 5 AA.	
AC	AAW33009;	
AC	25-MAR-2003 (revised)	
DT	02-APR-1993 (first entry)	
XX	Alpha-substituted short peptide.	
DE	Alpha-substituted short peptide.	
XX	CCK; neuropeptide; endorphin; hormone; LHRH; contrareception; analgesia;	
KW	improved bioavailability.	
XX	Synthetic.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Modified-size 4	/note= "alpha-Me-Leu"
FT	Modified-size 5	/note= "Met-NH2"
XX		
PN	WO9219254-A1.	
XX	12-NOV-1992.	
PD	15-APR-1992; 92WO-US003119.	
XX		
PF	24-APR-1991; 91US-00690755.	
XX	20-MAR-1992; 92US-00852086.	
PR	(WARN) WARNER LAMBERT CO.	
PA	Horwell DC, Hughes J, Richardson RS, Howson W;	
XX	WPI; 1992-398522/48.	
DR		
XX	New alpha-substd. polypeptide are e.g. selective receptor ligands - for	
FT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX		
PS	Claim 3; Page 41; 46pp; English.	
XX	The peptide is a specifically claimed example of a group of generically	
CC	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	

CC may improve the activity of the peptide as a drug. Depending on the
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
 CC peptide, etc.), the modified peptides are variously useful for treating
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
 CC addictive drug withdrawal symptoms, hypertension, heart failure,
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
 CC asthma, bladder dysfunction, psychosis and arthritis; and as
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FFGLM 5
 DB 1 FFGLM 5

RESULT 2
 AAR33008
 ID AAR33008 standard; peptide; 5 AA.
 XX
 AC AAR33008;
 XX

DT 25-MAR-2003 (revised)
 DT 02-APR-1993 (first entry)
 XX
 XX

DE Alpha-substituted short peptide.
 XX

KM CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 XX improved bioavailability.
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 2 /note= "alpha-Me-Phe"
 FT Modified-site 5 /note= "Met-NH2"
 FT
 PN WO9219254-A1.

PD 12-NOV-1992.
 XX

PF 15-APR-1992; 92WO-US003119.
 XX

PR 24-APR-1991; 91US-00690755.
 PR 20-MAR-1992; 92US-00852086.
 XX

PA (WARN) WARNER LAMBERT CO.
 XX

PI Horwell DC, Hughes J, Richardson RS, Howson W;
 PI
 DR WPI; 1992-398522/48.
 XX

PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
 PT depression, cancer, asthma, psychosis, arthritis, etc.
 XX

PS Claim 3; Page 41; 46pp; English.
 XX

CC The peptide is a specifically claimed example of a group of generically
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
 CC substituent on an alpha-C atom in the chain. Such substitution may modify
 CC the bioavailability, stability or absorbability of the peptide and hence
 CC may improve the activity of the peptide as a drug. Depending on the
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
 CC peptide, etc.), the modified peptides are variously useful for treating
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,

CC addictive drug withdrawal symptoms, hypertension, heart failure,
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
 CC asthma, bladder dysfunction, psychosis and arthritis; and as
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FFGLM 5
 DB 1 FFGLM 5

RESULT 3
 AAR33007
 ID AAR33007 standard; peptide; 5 AA.
 XX
 AC AAR33007;
 XX

DT 25-MAR-2003 (revised)
 DT 02-APR-1993 (first entry)
 XX
 XX

DE Alpha-substituted short peptide.
 XX

KM CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 KM Improved bioavailability.
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 1 /note= "alpha-Me-Phe"
 FT Modified-site 5 /note= "Met-NH2"
 FT
 PN WO9219254-A1.

PD 12-NOV-1992.
 XX

PF 15-APR-1992; 92WO-US003119.
 XX

PR 24-APR-1991; 91US-00690755.
 PR 20-MAR-1992; 92US-00852086.
 XX

PA (WARN) WARNER LAMBERT CO.
 XX

PI Horwell DC, Hughes J, Richardson RS, Howson W;
 PI
 DR WPI; 1992-398522/48.
 XX

PT New alpha-substd. polypeptide are e.g. selective receptor ligands - for
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
 PT depression, cancer, asthma, psychosis, arthritis, etc.
 XX

PS Claim 3; Page 41; 46pp; English.
 XX

CC The peptide is a specifically claimed example of a group of generically
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
 CC substituent on an alpha-C atom in the chain. Such substitution may modify
 CC the bioavailability, stability or absorbability of the peptide and hence
 CC may improve the activity of the peptide as a drug. Depending on the
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
 CC peptide, etc.), the modified peptides are variously useful for treating
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
 CC addictive drug withdrawal symptoms, hypertension, heart failure,
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
 CC asthma, bladder dysfunction, psychosis and arthritis; and as
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:09:53 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BL0SUM62
Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	66.7	5	2	PT0278
2	14	51.9	5	2	A44955
3	12	44.4	4	2	UQ1273
4	11	40.7	5	2	A61445
5	10	37.0	4	2	PT0240
6	10	37.0	4	2	A53284
7	10	37.0	5	2	G44817
8	10	37.0	5	2	T44817
9	10	37.0	5	2	E44817
10	10	37.0	5	2	C44817
11	10	37.0	5	2	A44817
12	10	37.0	5	2	A44817
13	9	33.3	5	2	A32516
14	9	33.3	5	2	PQ0689
15	9	33.3	5	2	B61445
16	8	29.6	4	2	PT0633
17	8	29.6	5	2	PT0572
18	7	25.9	3	3	B23751
19	7	25.9	4	2	E44823
20	7	25.9	4	2	B53284
21	7	25.9	5	2	T10954
22	7	25.9	5	2	JH0253
23	6	22.2	3	3	PT0636
24	6	22.2	3	3	PT0571
25	6	22.2	3	3	GKHU
26	6	22.2	3	3	A60898
27	6	22.2	3	3	A23751
28	6	22.2	4	1	ECXAA
29	6	22.2	4	1	ECXAA

30	6	22.2	4	2	D41654	hypothetical prote
31	6	22.2	4	2	S53508	searvation-induced
32	6	22.2	4	2	T30569	hypothetical prote
33	6	22.2	4	2	T38888	COI intron 16 prot
34	6	22.2	4	2	A25844	autho-RF amide neu
35	6	22.2	4	2	A34626	RFCH-related neuro
36	6	22.2	4	2	S39390	myosin-IIght-chain
37	6	22.2	4	2	S43959	ig mu chain V regl
38	6	22.2	4	2	S47552	ubiquitin - rat
39	6	22.2	4	2	S09478	globulin IV alpha
40	6	22.2	4	2	PL0140	carbon-monoxide de
41	6	22.2	4	2	A35779	neuropeptide Antho
42	6	22.2	4	2	A60418	FMRFamide - polych
43	6	22.2	4	2	A32480	achatin-I - giant
44	6	22.2	4	2	PT0271	ig heavy chain CRD
45	6	22.2	4	2	PT0711	T-cell receptor be

ALIGNMENTS

RESULT 1
PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0278
R/Yamada, M.; Maserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0278
A/Molecule type: DNA
A/Residues: 1-5 <YAM>
A/Cross-references: UNIPARC:UPI000017C202
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 18; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGIM 5
DB 1 YFGVL 5
RESULT 2
A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)
C/Species: Vibrio harveyi
C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C/Accession: A44955
R/Paguet, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A/Title: Chemical modification and characterization of the alpha cyteine 106 at the Vib
A/Reference number: A44955; MUID:90175700; PMID:2626493
A/Accession: A44955
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <PAO>
C/Keywords: FMN; luminescence; monooxygenase; oxidoreductase
Query Match 51.9%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGL 4
DB 1 FGI 3

```
RESULT 3
JQ1273
neuropeptide Antho-Kamide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C>Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 05-Jul-2004
C:Accession: JQ1273
R:Nochackx, H.P.; Rinehart, K.L.; Grimmelikhuijsen, C.J.P.
Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A>Title: Isolation of L-3-phenylactic-Phe-Lys-Ala-NH2 (Antho-Kamide), a novel neuropep
A:Reference number: JQ1273; MUID:92028852; PMID:1681803
A:Accession: JQ1273
A:Molecule type: protein
A:Residues: 1-4 <NOT>
A:Cross-references: UNIPROT:P58705; UNIPARC:UPI000012A703
C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following glyco
C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation
F:1/Modified site: L-3-phenylactic acid (Phe) #status experimental
F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match          44.4%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
Db 1 FF 2

RESULT 4
A61445
Met-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A61445
R:leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A>Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MUID:84144823; PMID:6583690
A:Accession: A61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Cross-references: UNIPARC:UPI000002CF9B
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match          40.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GLM 5
Db 3 GLM 5

RESULT 5
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0223; MUID:91108337; PMID:1899102
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Cross-references: UNIPARC:UPI000017C1E2
A:Experimental source: B lymphocyte
C:Keywords: heterodimer; immunoglobulin

Query Match          37.0%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

QY 3 GL 4
Db 3 GL 4

RESULT 6
A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A>Title: Evolutionarily conserved organization and sequences of germline diversity and j
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: A53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: UNIPARC:UPI000011E8F2; GB:S60737; NID:9233916; PIDN:AB19517.1; PID:
A>Note: sequence extracted from NCBI backbone (NCBI:60737, NCBI:60739)
C:Keywords: T-cell receptor

Query Match          37.0%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4
Db 1 GL 2

RESULT 7
G44817
27.5 kDa structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: G44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A>Title: Lysozyme in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: G44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Cross-references: UNIPARC:UPI000017CA3A
A>Note: sequence extracted from NCBI backbone (NCBI:70333)

Query Match          37.0%; Score 10; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4
Db 4 GL 5

RESULT 8
I44817
27.5K structural protein - Leuconostoc oenos phage P37 (fragment)
C:Species: Leuconostoc oenos phage P37
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: I44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A>Title: Lysozyme in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: I44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Cross-references: UNIPARC:UPI000017CA3A
```

```
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4
Db 3 GL 4

RESULT 6
A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A>Title: Evolutionarily conserved organization and sequences of germline diversity and j
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: A53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: UNIPARC:UPI000011E8F2; GB:S60737; NID:9233916; PIDN:AB19517.1; PID:
A>Note: sequence extracted from NCBI backbone (NCBI:60737, NCBI:60739)
C:Keywords: T-cell receptor

Query Match          37.0%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4
Db 1 GL 2

RESULT 7
G44817
27.5 kDa structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: G44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A>Title: Lysozyme in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: G44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Cross-references: UNIPARC:UPI000017CA3A
A>Note: sequence extracted from NCBI backbone (NCBI:70333)

Query Match          37.0%; Score 10; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4
Db 4 GL 5

RESULT 8
I44817
27.5K structural protein - Leuconostoc oenos phage P37 (fragment)
C:Species: Leuconostoc oenos phage P37
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: I44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A>Title: Lysozyme in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: I44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Cross-references: UNIPARC:UPI000017CA3A
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:06:57 ; Search time 225 Seconds
(without alignments)
15.678 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	59.3	5	1 AL14 CARMA	P81817 carcinus ma
2	12	44.4	4	1 PFKA ANTEL	P58705 antiopeura
3	12	44.4	4	1 OCP1 OCTMI	P58648 octopus min
4	12	44.4	5	1 PAP2 PARMA	P81864 pardachirus
5	12	44.4	5	1 RBE1 LITRU	P82070 litoria rub
6	12	44.4	5	1 RBE2 LITRU	P82071 litoria rub
7	12	44.4	5	1 RBE3 LITRU	P82072 litoria rub
8	12	44.4	5	1 RBE3 LITRU	P82073 litoria rub
9	12	44.4	5	1 UC22 MAIZE	P80628 zea mays (m
10	11	40.7	5	1 TPIS CANFA	P54714 canis famli
11	9	33.3	4	1 FYRI ANTEL	P58706 antiopeura
12	9	33.3	4	1 IIME SEROF	P83568 sepia offic
13	7	25.9	5	1 UP01 MOUSE	P18639 mus musculu
14	6	22.2	2	1 GMA SEROF	P83570 sepia offic
15	6	22.2	3	1 GRWV HUMAN	P01157 homo sapien
16	6	22.2	4	1 ACHI ACHFU	P35904 achactina fu
17	6	22.2	4	1 DCML PSECH	P19916 pseudomonas
18	6	22.2	4	1 BOS1 HUMAN	P02731 homo sapien
19	6	22.2	4	1 FAR3 HIRME	P42562 hirudo medi
20	6	22.2	4	1 FAR4 HIRME	P42563 hirudo medi
21	6	22.2	4	1 FLRF HELTI	P69138 helisoma tr
22	6	22.2	4	1 FLRF HELTI	P69137 hirudo medi
23	6	22.2	4	1 FLRN ANTEL	P58707 antiopeura
24	6	22.2	4	1 FMRF HELTI	P69148 helisoma tr
25	6	22.2	4	1 FMRF HIRME	P69147 hirudo medi
26	6	22.2	4	1 FMRF MACNI	P69145 macrocallis
27	6	22.2	4	1 FMRF NERYI	P69146 nereis vire
28	6	22.2	4	1 OCP3 OCTMI	P58649 octopus min
29	6	22.2	4	1 TPAN1 PANIM	P84465 pandinus im
30	6	22.2	4	2 O16047 HUMAN	O16047 homo sapien
31	6	22.2	5	1 AP21 EISRO	P61182 eisenia foe

32	6	22.2	5	1 E103 LITRU	P82099 litoria rub
33	6	22.2	5	1 E104 LITRU	P82100 litoria rub
34	6	22.2	5	1 FARP ARTTR	P41853 artiopechi
35	6	22.2	5	1 FARP CHICK	P83308 gallus gall
36	6	22.2	5	1 SUGA ACHDO	P19991 acheta dome
37	6	22.2	5	1 UXA4 CHLTR	P38005 chlamydia t
38	5	18.5	4	1 DCMS PSECH	P19918 pseudomonas
39	5	18.5	4	2 Q96AT0 HUMAN	Q96AT0 homo sapien
40	5	18.5	5	1 B10A CTRFR	P13071 citrobacter
41	5	18.5	5	1 B10B CTRFR	P12997 citrobacter
42	5	18.5	5	1 RPC2 BPR21	P69203 bacterioph
43	5	18.5	5	2 Q99007 HORVU	Q99007 hordeum vul
44	5	18.5	5	2 P83073 BACCE	P83073 bacillus ce
45	4	14.8	4	1 TPAN2 PANIM	P84464 pandinus im

ALIGNMENTS

RESULT 1	AL14 CARMA	STANDARD	PRT	5 AA
ID	AL14 CARMA	STANDARD	PRT	5 AA
AC	P81817			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Carcinus maenas (Common shore crab)			
OS	Carcinus maenas (Common shore crab) (Green crab)			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eubrachyura; Portunoidae; Portunidae; Carcinus.			
OX	NCBI_TaxID=6759;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RC	TISSUE=Cerebral ganglion, and Thoracic ganglion;			
RX	MEDLINE=98121193; PubMed=9461295;			
RA	Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,			
RA	Thorpe A.;			
RT	"Isolation and identification of multiple neuropeptides of the			
RT	allatostatin superfamily in the shore crab Carcinus maenas."			
RL	Eur. J. Biochem. 250:727-734(1997).			
CC	-1- FUNCTION: May act as a neurotransmitter or neuromodulator.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the allatostatin family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
KW	Amidation; Direct protein sequencing; Multigene family; Neuropeptide.			
FT	MOD RES 5			
FT	MOD RES 5			
SO	SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;			
QY	Query Match	59.3%;	Score 16;	DB 1; Length 5;
QY	Best Local Similarity	100.0%;	Pred. No. 2.2e+6;	Potential
QY	Matches 3;	Conservative 0;	Mismatches 0;	Indels 0;
QY	2 FGL 4			
QY	3 FGL 5			
DB				
RESULT 2	PFKA ANTEL	STANDARD	PRT	4 AA
ID	PFKA ANTEL	STANDARD	PRT	4 AA
AC	P58705			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Antho-Kamide.			
OS	Antiopeura elegantissima (Sea anemone).			

```

CC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
CC Nyantheae; Actinidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenylalanyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211 (1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide."
RL Proc. R. Soc. Lond. B, Biol. Sci. 253:183-188 (1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: J01273; J01273.
KM Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1
FT MOD_RES 4 4 Alanine amide.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 1 FF 2

RESULT 3
OCPI_OCTMI STANDARD; PRT; 4 AA.
AC PS6648:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RT Tissue=Brain;
RX MEDLINE=20333615; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor."
RL Peptides 21:623-630 (2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC than Ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC D-amino acid; Direct protein sequencing; Hormone.
KM MOD_RES 2 2 D-phenylalanine (in form Ocp-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FG 3
DB 2 FG 3

RESULT 4
PAP2_PAPMA STANDARD; PRT; 5 AA.
ID PAP2_PAPMA
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorphi; Acanthopterygii; Percormorpha; Pleuronectiformes;
CC Soleioidi; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT marmoratus)."
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SIMILARITY: Belongs to the pardaxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KM Direct protein sequencing; Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 2 FF 3

RESULT 5
RBE11_LITRU STANDARD; PRT; 5 AA.
ID RBE11_LITRU
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:07:07 : Search time 45 Seconds
(without alignments)
9.186 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 8265679 residues

Total number of hits satisfying chosen parameters: 30800

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	1	US-07-934-553-2
2	27	100.0	5	1	US-08-225-474-2
3	27	100.0	5	1	US-07-737-371E-6
4	27	100.0	5	2	US-09-265-690C-1
5	27	100.0	5	2	US-09-623-548A-604
6	27	100.0	5	2	US-10-134-187-3
7	27	100.0	5	2	US-09-657-276-604
8	24	88.9	5	1	US-07-737-371E-47
9	22	81.5	5	1	US-07-737-371E-49
10	22	81.5	5	1	US-08-441-591-63
11	21	77.8	4	1	US-08-303-362A-63
12	21	77.8	4	2	US-09-265-690C-2
13	21	77.8	4	2	US-09-635-266-3
14	21	77.8	4	2	US-10-230-133-3
15	21	77.8	4	2	US-09-623-548A-623
16	21	77.8	4	2	US-10-695-536-3
17	21	77.8	4	2	US-09-657-276-623
18	21	77.8	4	4	PCT-US95-05600-80
19	21	77.8	5	1	US-08-070-301-6
20	21	77.8	5	2	US-09-623-548A-565
21	21	77.8	5	2	US-09-657-276-565
22	20	74.1	5	1	US-07-753-909B-3
23	20	74.1	5	1	US-08-269-288-1
24	20	74.1	5	1	US-08-391-910-1
25	20	74.1	5	1	US-08-418-994-1
26	20	74.1	5	1	US-08-391-814-1
27	20	74.1	5	1	US-08-391-814-1

28	20	74.1	5	1	US-08-441-591-61	Sequence 61, Appl
29	20	74.1	5	1	US-08-303-362A-61	Sequence 61, Appl
30	20	74.1	5	1	US-08-463-874-1	Sequence 1, Appl
31	20	74.1	5	1	US-08-444-135-1	Sequence 1, Appl
32	20	74.1	5	1	US-08-318-391-1	Sequence 1, Appl
33	20	74.1	5	2	US-08-257-966-1	Sequence 4, Appl
34	20	74.1	5	2	US-09-265-690C-4	Sequence 1, Appl
35	20	74.1	5	2	US-08-153-847-1	Sequence 1, Appl
36	20	74.1	5	2	US-09-635-266-4	Sequence 4, Appl
37	20	74.1	5	2	US-10-230-133-4	Sequence 4, Appl
38	20	74.1	5	2	US-10-695-536-4	Sequence 4, Appl
39	20	74.1	5	2	US-10-668-565-1	Sequence 1, Appl
40	20	74.1	5	4	PCT-US95-05600-78	Sequence 78, Appl
41	20	74.1	4	2	US-08-722-126A-20	Sequence 20, Appl
42	19	70.4	5	1	US-08-765-061-5	Sequence 5, Appl
43	19	70.4	5	2	US-09-623-548A-606	Sequence 606, App
44	19	70.4	5	2	US-09-657-276-606	Sequence 606, App
45	19	70.4	5	2	US-09-657-276-606	Sequence 606, App

ALIGNMENTS

```
RESULT 1
US-07-934-553-2
: Sequence 2, Application US/07934553
: Patent No. 5314690
: GENERAL INFORMATION:
: APPLICANT: PATTERSON, ROY
: APPLICANT: HARRIS, KATHLEEN E
: TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
: TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLEGENS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: TILTON, FALLOM, LUNGWUS & CHESTNUT
: STREET: 100 SOUTH WACKER DRIVE
: CITY: CHICAGO
: STATE: ILLINOIS
: COUNTRY: USA
: ZIP: 60606-4002
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/934,553
: FILING DATE: 19920821
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/705,071
: FILING DATE: 24-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: FENTRESS, SUSAN B
: REGISTRATION NUMBER: 31,327
: REFERENCE/DOCKET NUMBER: NU-90333CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/456-8000
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: AMINO ACID
: STRADEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-07-934-553-2
:
: Query Match 100.0%; Score 27; DB 1; Length 5;
: Best Local Similarity 100.0%; Pred. No. 4.6e+05;
: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 1 PFGLM 5

RESULT 2

US-08-225-474-2
Sequence 2, Application US/08225474

Patent No. 5560915

GENERAL INFORMATION:

APPLICANT: Patterson, Roy

APPLICANT: Harris, Kathleen E.

TITLE OF INVENTION: Method and Composition for Treating

TITLE OF INVENTION: 198 Mediated Allergies

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut

STREET: 100 S. Wacker Drive, Suite 960

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-4002

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/225,474

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,553

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/705,071

FILING DATE: 24-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Tilton, Timothy L.

REGISTRATION NUMBER: 16,926

REFERENCE/DOCKET NUMBER: NU 9033-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)-456-8000

TELEFAX: (312)-456-7776

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-225-474-2

Query Match

Best Local Similarity 100.0%; Score 27; DB 1; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5

Db 1 PFGLM 5

US-07-737-371E-6

Sequence 6, Application US/07737371E

Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E

FILING DATE: 29-JUL-1991

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/559,172

FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00108/028002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-737-371E-6

Query Match

Best Local Similarity 100.0%; Score 27; DB 1; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5

Db 1 PFGLM 5

US-09-265-690C-1

Sequence 1, Application US/09265690C

Patent No. 6372440

GENERAL INFORMATION:

APPLICANT: Wells, Ibert

TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma

TITLE OF INVENTION: for Disease Diagnosis

FILE REFERENCE: 1427001

CURRENT APPLICATION NUMBER: US/09/265,690C

CURRENT FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 5

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MOD RES

LOCATION: (5)..(5)

OTHER INFORMATION: AMIDATION

US-09-265-690C-1

Query Match

Best Local Similarity 100.0%; Score 27; DB 2; Length 5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5

Db 1 PFGLM 5

US-07-737-371E-6

Sequence 6, Application US/07737371E

Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.

TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:17:08 ; Search time 158 Seconds
(without alignments)
13.222 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 31220

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	US-09-265-690C-1	Sequence 1, Appli
2	27	100.0	5	US-10-053-669-1	Sequence 1, Appli
3	27	100.0	5	US-10-134-187-3	Sequence 3, Appli
4	27	100.0	5	US-10-688-741-3	Sequence 3, Appli
5	27	100.0	5	US-10-805-881-1	Sequence 1, Appli
6	27	100.0	5	US-10-720-039-3	Sequence 3, Appli
7	27	100.0	5	US-10-497-628-15	Sequence 15, Appli
8	27	100.0	5	US-11-066-697-604	Sequence 604, App
9	27	100.0	5	US-11-025-494-3	Sequence 3, Appli
10	24	88.9	5	US-10-497-628-16	Sequence 16, Appli
11	22	81.5	4	US-10-821-240A-270	Sequence 270, App
12	21	77.8	4	US-09-265-690C-2	Sequence 2, Appli
13	21	77.8	4	US-10-230-133-3	Sequence 3, Appli
14	21	77.8	4	US-10-053-669-2	Sequence 2, Appli
15	21	77.8	4	US-10-695-536-3	Sequence 3, Appli
16	21	77.8	4	US-10-805-881-2	Sequence 2, Appli
17	21	77.8	4	US-10-497-628-2	Sequence 2, Appli
18	21	77.8	4	US-11-018-630-3	Sequence 3, Appli
19	21	77.8	4	US-11-066-697-623	Sequence 623, App
20	21	77.8	5	US-10-346-737A-30	Sequence 30, Appli
21	21	77.8	5	US-10-497-628-17	Sequence 17, Appli
22	21	77.8	5	US-11-066-697-565	Sequence 565, App
23	20	74.1	5	US-09-265-690C-4	Sequence 4, Appli
24	20	74.1	5	US-10-230-133-4	Sequence 4, Appli
25	20	74.1	5	US-10-053-669-4	Sequence 4, Appli
26	20	74.1	5	US-10-695-536-4	Sequence 4, Appli
27	20	74.1	5	US-10-805-881-4	Sequence 4, Appli

28	20	74.1	5	US-10-451-304-12	Sequence 12, Appli
29	20	74.1	5	US-11-018-690-4	Sequence 4, Appli
30	19	70.4	5	US-10-346-737A-22	Sequence 22, Appli
31	19	70.4	5	US-11-066-697-606	Sequence 606, App
32	18	66.7	3	US-11-066-697-1527	Sequence 1527, App
33	18	66.7	4	US-08-484-409-14	Sequence 14, Appli
34	18	66.7	4	US-10-155-170-4	Sequence 4, Appli
35	18	66.7	4	US-10-351-641-826	Sequence 826, App
36	18	66.7	4	US-10-822-661-4	Sequence 4, Appli
37	18	66.7	4	US-10-821-240A-298	Sequence 298, App
38	18	66.7	4	US-10-878-175B-3	Sequence 3, Appli
39	18	66.7	5	US-09-920-306-38	Sequence 38, Appli
40	17	63.0	5	US-10-168-789A-32	Sequence 32, Appli
41	17	63.0	5	US-10-783-311-299	Sequence 299, App
42	16	59.3	4	US-09-879-442A-9	Sequence 9, Appli
43	16	59.3	5	US-09-886-135-2	Sequence 2, Appli
44	16	59.3	5	US-10-620-052A-45	Sequence 45, Appli
45	16	59.3	5	US-10-357-105-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-265-690C-1
; Sequence 1, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

Query Match 100.0%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGIM 5
|||||
Db 1 FFGIM 5

RESULT 2
US-10-053-669-1
; Sequence 1, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-10-053-669-1
```

```
Query Match          100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FFGLM 5
        |||||
Db       1 FFGLM 5
```

```
RESULT 3
US-10-134-187-3
; Sequence 3, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/134,187
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-134-187-3
```

```
Query Match          100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FFGLM 5
        |||||
Db       1 FFGLM 5
```

```
RESULT 4
US-10-688-741-3
; Sequence 3, Application US/10688741
; Publication No. US20040106636A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/688,741
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-688-741-3
```

```
Query Match          100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FFGLM 5
        |||||
Db       1 FFGLM 5
```

```
RESULT 5
US-10-805-881-1
; Sequence 1, Application US/10805881
; Publication No. US20040171093A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert C.
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
; FILE REFERENCE: 800812-0005
; CURRENT APPLICATION NUMBER: US/10/805,881
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 10/053,669
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 10/695,536
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-10-805-881-1
```

```
Query Match          100.0%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FFGLM 5
        |||||
Db       1 FFGLM 5
```

```
RESULT 6
US-10-720-039-3
; Sequence 3, Application US/10720039
; Publication No. US20040259786A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Transporting A Chimeric Hybrid Molecule Across The Bloo
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/720,039
; CURRENT FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-720-039-3
```

```
Query Match          100.0%; Score 27; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 FFGLM 5
        |||||
Db       1 FFGLM 5
```

```
RESULT 7
US-10-497-628-15
; Sequence 15, Application US/10497628
; Publication No. US20050009752A1
; GENERAL INFORMATION:
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:17:59 ; Search time 8 Seconds
(without alignments)
1.694 Million cell updates/sec

Title: US-10-805-881-1
Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 220

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	44.4	4	US-11-064-785-1	Sequence 1, Appli
2	12	44.4	5	US-11-016-706-52	Sequence 52, Appl
3	12	44.4	5	US-11-021-441-62	Sequence 52, Appl
4	10	37.0	4	US-11-046-456-27	Sequence 27, Appl
5	10	37.0	4	US-11-046-644-27	Sequence 27, Appl
6	10	37.0	4	US-11-052-168A-38	Sequence 38, Appl
7	10	37.0	5	US-10-502-145-32	Sequence 32, Appl
8	10	37.0	5	US-10-726-554-12	Sequence 12, Appl
9	9	33.3	5	US-10-997-066-17	Sequence 17, Appl
10	9	33.3	5	US-11-035-682-13	Sequence 13, Appl
11	9	33.3	5	US-11-079-969-2	Sequence 2, Appl
12	9	33.3	5	US-11-054-515-3167	Sequence 3167, Ap
13	9	33.3	5	US-11-187-989-7	Sequence 7, Appl
14	7	25.9	4	US-10-977-367-21	Sequence 21, Appl
15	7	25.9	4	US-10-977-367-36	Sequence 36, Appl
16	7	25.9	4	US-10-997-066-16	Sequence 16, Appl
17	7	25.9	4	US-10-966-648-28	Sequence 28, Appl
18	7	25.9	4	US-11-035-682-12	Sequence 12, Appl
19	7	25.9	4	US-11-113-224-57	Sequence 57, Appl
20	7	25.9	4	US-11-113-224-59	Sequence 59, Appl
21	7	25.9	5	US-10-977-367-22	Sequence 22, Appl
22	7	25.9	5	US-10-977-367-24	Sequence 24, Appl
23	7	25.9	5	US-10-977-367-37	Sequence 37, Appl
24	7	25.9	5	US-10-990-627-10	Sequence 10, Appl
25	7	25.9	5	US-11-053-100-4	Sequence 4, Appl

26	7	25.9	5	US-11-053-100-5	Sequence 5, Appli
27	7	25.9	5	US-11-053-100-6	Sequence 6, Appli
28	7	25.9	5	US-11-054-515-2210	Sequence 2210, Ap
29	7	25.9	5	US-11-054-515-3174	Sequence 3174, Ap
30	6	22.2	3	US-11-052-168A-4	Sequence 4, Appli
31	6	22.2	3	US-11-052-168A-39	Sequence 39, Appl
32	6	22.2	4	US-10-503-575-48	Sequence 48, Appl
33	6	22.2	4	US-10-503-575-49	Sequence 49, Appl
34	6	22.2	4	US-10-503-575-59	Sequence 59, Appl
35	6	22.2	4	US-10-503-575-62	Sequence 62, Appl
36	6	22.2	4	US-10-977-367-1	Sequence 1, Appli
37	6	22.2	4	US-10-979-821-77	Sequence 77, Appli
38	6	22.2	4	US-10-939-890-8	Sequence 8, Appli
39	6	22.2	4	US-10-939-890-18	Sequence 18, Appl
40	6	22.2	4	US-10-939-890-262	Sequence 262, App
41	6	22.2	4	US-10-939-890-420	Sequence 420, App
42	6	22.2	4	US-10-939-890-490	Sequence 490, App
43	6	22.2	4	US-10-939-890-791	Sequence 791, App
44	6	22.2	4	US-10-939-890-792	Sequence 792, App
45	6	22.2	4	US-10-939-890-871	Sequence 871, App

ALIGNMENTS

RESULT 1
US-11-064-785-1
Sequence 1, Application US/11064785
Publication No. US20050256030A1
GENERAL INFORMATION:
APPLICANT: FENG, BAINIAN
TITLE OF INVENTION: HETEROCYCLIC SELF-IMMOLATIVE LINKERS AND
TITLE OF INVENTION: CONTIGATES
FILE REFERENCE: 39766-0143A
CURRENT FILING DATE: US/11/064, 785
PRIOR APPLICATION NUMBER: 2005-02-22
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ. ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-11-064-785-1
Query Match 44.4%; Score 12; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
Gy 1 FFG 3
Db 2 FLG 4
RESULT 2
US-11-016-706-52
Sequence 52, Application US/11016706
Publication No. US20050244334A1
GENERAL INFORMATION:
APPLICANT: CASTILLO, GERARDO
APPLICANT: LAKE, THOMAS P.
APPLICANT: NGUYEN, BETH P.
APPLICANT: SANDERS, VIRGINIA J.
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
FILE REFERENCE: PROTO. P03C13
CURRENT APPLICATION NUMBER: US/11/016, 706
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 09/962, 955

;; PRIOR FILING DATE: 2001-09-24
;; PRIOR APPLICATION NUMBER: 09/938,275
;; PRIOR FILING DATE: 2001-08-22
;; PRIOR APPLICATION NUMBER: 08/947,057
;; PRIOR FILING DATE: 1997-10-08
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO: 52
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-11-016-706-52

Query Match 44.4%; Score 12; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FF 2
||
Db 3 FF 4

RESULT 3
US-11-021-441-62
;; Sequence 62, Application US/11021441
;; Publication No. US20050249748A1
;; GENERAL INFORMATION:
;; APPLICANT: DUBENSKY, Thomas W., Jr.
;; APPLICANT: PORTNOY, Daniel A.
;; APPLICANT: LUCKETT, William S., Jr.
;; APPLICANT: COOK, David N.
;; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
;; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: 282172003900
;; CURRENT APPLICATION NUMBER: US/11/021,441
;; CURRENT FILING DATE: 2004-12-23
;; PRIOR APPLICATION NUMBER: US 60/616,750
;; PRIOR FILING DATE: 2004-10-06
;; PRIOR APPLICATION NUMBER: US 60/615,287
;; PRIOR FILING DATE: 2004-10-01
;; PRIOR APPLICATION NUMBER: US 60/599,377
;; PRIOR FILING DATE: 2004-08-05
;; PRIOR APPLICATION NUMBER: PCT/US2004/23881
;; PRIOR FILING DATE: 2004-07-23
;; PRIOR APPLICATION NUMBER: US 10/883,599
;; PRIOR FILING DATE: 2004-06-30
;; PRIOR APPLICATION NUMBER: US 60/556,744
;; PRIOR FILING DATE: 2004-03-26
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 62
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Bacillus subtilis
US-11-021-441-62

Query Match 44.4%; Score 12; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FG 3
||
Db 4 FG 5

RESULT 4
US-11-046-456-27
;; Sequence 27, Application US/11046456
;; Publication No. US20050256044A1

;; GENERAL INFORMATION:
;; APPLICANT: Boyle, Bryan
;; APPLICANT: Funk, Walter
;; APPLICANT: Kakitani, Makoto
;; APPLICANT: Oshima, Takeshi
;; APPLICANT: Park, Eun Ju
;; APPLICANT: Tang, Y. Tom
;; APPLICANT: Yagi, Mikio
;; APPLICANT: Tomizuka, Kazuma
;; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
;; FILE REFERENCE: 18824-003001
;; CURRENT APPLICATION NUMBER: US/11/046,456
;; CURRENT FILING DATE: 2005-01-27
;; PRIOR APPLICATION NUMBER: US 60/539,605
;; PRIOR FILING DATE: 2004-01-27
;; PRIOR APPLICATION NUMBER: US 60/619,241
;; PRIOR FILING DATE: 2004-10-15
;; PRIOR APPLICATION NUMBER: US 10/488,423
;; PRIOR FILING DATE: 2004-03-03
;; PRIOR APPLICATION NUMBER: PCT/US02/27746
;; PRIOR FILING DATE: 2002-08-30
;; NUMBER OF SEQ ID NOS: 182
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 27
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-046-456-27

Query Match 37.0%; Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GLM 5
||
Db 2 GTM 4

RESULT 5
US-11-046-644-27
;; Sequence 27, Application US/1104644
;; Publication No. US20050256036A1
;; GENERAL INFORMATION:
;; APPLICANT: Boyle, Bryan
;; APPLICANT: Funk, Walter
;; APPLICANT: Kakitani, Makoto
;; APPLICANT: Oshima, Takeshi
;; APPLICANT: Park, Emily
;; APPLICANT: Tang, Y. Tom
;; APPLICANT: Tomizuka, Kazuma
;; APPLICANT: Yagi, Mikio
;; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
;; FILE REFERENCE: 11926-194001
;; CURRENT APPLICATION NUMBER: US/11/046,644
;; CURRENT FILING DATE: 2005-01-27
;; PRIOR APPLICATION NUMBER: US 60/539,605
;; PRIOR FILING DATE: 2004-01-27
;; PRIOR APPLICATION NUMBER: US 60/619,241
;; PRIOR FILING DATE: 2004-10-15
;; NUMBER OF SEQ ID NOS: 178
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 27
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-046-644-27

Query Match 37.0%; Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GLM 5
||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:02:43 ; Search time 60.2857 Seconds
(without alignments)
29.153 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 990051

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2	AAW41683
2	21	100.0	4	2	AAV31075
3	21	100.0	4	3	AAAB23026
4	21	100.0	4	3	AAV67577
5	21	100.0	4	4	AAAB91447
6	21	100.0	4	5	ABBI0091
7	21	100.0	4	5	AAU77846
8	21	100.0	4	7	ADDE94198
9	21	100.0	4	8	ADRA43772
10	21	100.0	5	2	AAAR33009
11	21	100.0	5	2	AAAR33008
12	21	100.0	5	2	AAAR33007
13	21	100.0	5	2	AAAR33010
14	21	100.0	5	2	AAAR54549
15	21	100.0	5	2	AAAR54551
16	21	100.0	5	2	AAAR54550
17	21	100.0	5	2	AAAR54548
18	21	100.0	5	2	AAW41687
19	21	100.0	5	2	AAW99643
20	21	100.0	5	2	AAV50325
21	21	100.0	5	2	AAW92660
22	21	100.0	5	2	AAW92702
23	21	100.0	5	3	AAAB23025
24	21	100.0	5	3	AAV67576

25	21	100.0	5	4	AAAB91428	AAAB91428 Tachykinin
26	21	100.0	5	4	AAAB91389	AAAB91389 Tachykinin
27	21	100.0	5	5	ABBI0090	ABBI0090 Substance
28	21	100.0	5	5	ABBI0089	ABBI0089 Substance
29	21	100.0	5	5	ABBI0088	ABBI0088 Substance
30	21	100.0	5	5	AAU77845	AAU77845 Tachykinin
31	21	100.0	5	7	ADDE94205	ADDE94205 High actin
32	21	100.0	5	7	ADDE94203	ADDE94203 High actin
33	21	100.0	5	7	ADDE94204	ADDE94204 High actin
34	21	100.0	5	7	ADDE94205	ADDE94205 High actin
35	21	100.0	5	8	ADN95078	ADN95078 Mammalian
36	21	100.0	5	8	ADRO3603	ADRO3603 E. coli m
37	21	100.0	5	8	ADRA43771	ADRA43771 Human mag
38	21	100.0	5	9	ADVA4808	ADVA4808 Mammalian
39	21	100.0	6	1	AAAP40519	AAAP40519 Sequence
40	21	100.0	6	1	AAAP50694	AAAP50694 Sequence
41	21	100.0	6	1	AAAP50632	AAAP50632 Substance
42	21	100.0	6	1	AAAP61486	AAAP61486 Peptide h
43	21	100.0	6	2	AAAR07893	AAAR07893 Cyclopeptide
44	21	100.0	6	2	AAAR07899	AAAR07899 Cyclopeptide
45	21	100.0	6	2	AAAR21959	AAAR21959 Substance

ALIGNMENTS

RESULT 1	AAW41683	standard; peptide; 4 AA.
ID	AAW41683	
AC	AAW41683;	
DT	09-JUN-1998	(first entry)
DE	Peptide used in ophthalmic drug to treat corneal disorders.	
KW	Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye; keratitis; insulin like growth factor-I; IGF-I; eye drop.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Modified-site	4
FT		/note="C-terminal amide"
XX	W09749419-A1.	
XX	31-DEC-1997.	
XX	11-JUN-1997;	97WO-JP002015.
XX	26-JUN-1996;	96JP-00165612.
XX	(SANT) SANTEN PHARM CO LTD.	
XX	Nishida T, Nakamura M, Nakata K;	
XX	WPI; 1998-076907/07.	
XX	Ophthalmic drug composition containing tetra-peptide - is useful as	
XX	corneal disorder remedy for corneal ulcer, corneal epithelial peeling,	
XX	dry eye, keratitis.	
XX	Claim 1; Page 15; 19pp; Japanese.	
XX	The present sequence represents a tetrapeptide which is the active	
XX	ingredient in an ophthalmic drug composition. It is used, together with	
XX	insulin like growth factor-I (IGF-I), to treat corneal disorders such as	
XX	corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The	
XX	dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and	
XX	0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of	
XX	the composition is eye drops	

SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
 ||||
 1 FGLM 4

DB

RESULT 2
AAV31075

ID AAV31075 standard; peptide; 4 AA.

AC AAV31075;

DT 21-OCT-1999 (first entry)

DE Non-crosslinked protein particle peptide 124.

KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 albumin; haemoglobin; nanometer; micrometer; clearance.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"

XX US5945033-A.

XX 31-AUG-1999.

XX 12-NOV-1996; 96US-00747137.

XX 15-JAN-1991; 91US-00641720.

XX 13-OCT-1992; 92US-00959560.

XX 01-JUN-1993; 93US-00069831.

XX 14-MAR-1994; 94US-00212546.

XX (HEMO-) HEMOSPHERE INC.

XX Yen RCK;

XX WPI; 1999-508153/42.

XX Non-crosslinked protein particles for therapeutic and diagnostic use.

XX Example 22; Col 103-104; 65pp; English.

XX This invention describes a novel aqueous suspension of monodisperse

XX particles on non-crosslinked, non-denatured albumin (50-6000 nm) which is

XX stable against dissolving upon dilution with an alcohol-free aqueous

XX medium. The method involves (a) forming an aqueous solution containing

XX albumin and hemoglobin and (b) treating the aqueous solution with an

XX alcohol to cause the solution to become turbid. The particles are useful

XX as agents for in vivo administration, either of their own administration

XX or as a vehicle for other therapeutic or diagnostic agents. The method

XX permits the formation of albumin and hemoglobin particles in the

XX nanometer and micrometer size range, in a form closer to their natural

XX form than the forms of the prior art. The particles therefore constitute

XX a more closely controlled agent for in vivo administration, with greater

XX ease of clearance from the body after their period of usefulness.

XX CC AAV30952-73115 represent peptides used in the method of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
 ||||
 1 FGLM 4

DB 1 FGLM 4

RESULT 3

ID AAB23026 standard; peptide; 4 AA.

AC AAB23026;

DT 16-JAN-2001 (first entry)

DE Human/rat tachykinin Substance P C-terminal tetrapeptide.

KW Substance P; tachykinin; human; rat; magnesium binding defect;
 sodium sensitive essential hypertension; insulin resistance;

KW type 2 diabetes; antibody; immunoassay; quantification.

OS Homo sapiens.

OS Rattus sp.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"

XX WO200054053-A1.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US003707.

XX 10-MAR-1999; 99US-00265690.

XX (WEL/) WELLS I C.

XX Wells IC;

XX WPI; 2000-587457/55.

DR Detecting magnesium binding defects associated with abnormal
 physiological states such as sodium-sensitive essential hypertension and

PT type 2 insulin-resistant diabetes mellitus, comprises measuring a
 specific pentapeptide in blood.

PT Disclosure; Page 5; 21pp; English.

XX The invention relates to a method for detecting magnesium binding
 defects. The method comprises quantitating a tachykinin C-terminal

CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
 CC AAB23026) in blood using an antibody specific for the generalised

CC mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
 CC NH₂ (AAB23028). The method is useful for detecting cellular magnesium

CC binding defects which are associated with abnormal physiological states
 CC such as sodium-sensitive essential hypertension and type 2 diabetes

CC mellitus. The present sequence represents the C-terminal 4 amino acids of
 CC the tachykinin Substance P (AAB23027) from human and rat. This is a

CC degradation product of the Substance P C-terminal pentapeptide (AAB23025)
 CC and may also be assayed according to the method of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
 ||||
 1 FGLM 4

DB

RESULT 4
AAV67577

ID AAV67577 standard; peptide; 4 AA.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:18:04 ; Search time 16 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-10-805-881-2
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 A60654	substance P - guin
2	21	100.0	11	1 SPHO	substance P - hors
3	21	100.0	11	2 JN0023	substance P - chic
4	21	100.0	11	2 S33300	probable substance
5	21	100.0	11	2 E60409	substance P-like P
6	21	100.0	11	2 F60409	substance P-like P
7	21	100.0	11	2 S23308	substance P - rain
8	21	100.0	19	2 P60332	phospholipase A2 (
9	18	85.7	10	2 B49581	slalokinin II - ye
10	18	85.7	10	2 B61033	ranatachykinin B -
11	18	85.7	10	2 A49581	slalokinin I - yel
12	18	85.7	10	2 A24867	scylliorhinin I - s
13	18	85.7	11	2 S07203	uperolein - frog (
14	18	85.7	11	2 S07201	physalaemin - frog
15	18	85.7	11	2 A61033	ranatachykinin A -
16	17	81.0	26	2 A34280	phospholipase A2 (
17	17	81.0	27	2 B44180	phospholipase A2 (
18	16	76.2	8	2 D47393	neuropeptide cala
19	16	76.2	10	2 F60527	spirm-activating P
20	16	76.2	10	2 B60589	spirm-activating P
21	16	76.2	12	2 S01749	collagen alpha 1(I
22	16	76.2	12	2 PA0098	ribosomal protein
23	16	76.2	12	2 S07436	tachykinin - Afri
24	16	76.2	16	2 A47393	neuropeptide cala
25	16	76.2	17	2 S50901	chlorophyll a/b-bi
26	16	76.2	18	2 I52651	brain-derived neur
27	16	76.2	18	2 B44995	alkanal monooxygen
28	16	76.2	22	2 A35418	brain natriuretic
29	16	76.2	22	2 JN0910	N4-(beta-N-acetyl)lg

30	16	76.2	27	2 T17067	NADH2 dehydrogenas
31	16	76.2	27	2 S09734	photosystem I prot
32	16	76.2	27	2 S55802	srp protein (Baker
33	16	76.2	27	2 S55801	srp protein (Baker
34	16	76.2	28	2 F00691	photosystem I 5.6k
35	16	76.2	28	2 S49924	srp protein (Baker
36	16	76.2	28	2 T06925	hypothetical prote
37	16	76.2	29	2 S07055	photosystem I prot
38	16	76.2	29	2 S08088	gene VII protein -
39	16	76.2	30	2 B44314	intracisternal A p
40	16	76.2	30	2 T58367	gag protein - mous
41	16	76.2	30	2 S02088	blood group Rh-rel
42	16	76.2	30	2 E95079	hypothetical prote
43	15	71.4	5	2 PT0278	ig heavy chain CRD
44	15	71.4	10	1 SPPGMR	neuromedin K - pig
45	15	71.4	10	2 JN0024	neurokinin A - chi

ALIGNMENTS

RESULT 1

A60654
substance P - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A60654
R:Murphy, R.
Neuropeptides 14, 105-110, 1989
A:Title: Primary amino acid sequence of guinea-pig substance P.
A:Reference number: A60654; PMID:90044685; PMID:2478925
A:Accession: A60654
A:Molecule type: protein
A:Residues: 1-11 <MUR>
A:Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F,11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Query Local Similarity 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

SPHO
substance P - horse
C:Species: Equus caballus (domestic horse)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A01558
R:Studer, R.O.; Trzeciak, A.; Lengler, W.
Helv. Chim. Acta 56, 860-865, 1973
A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A:Reference number: A01558
A:Accession: A01558
A:Molecule type: protein
A:Residues: 1-11 <STU>
A:Cross-references: UNIPROT:P01290; UNIPARC:UPI000002BD74
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; hormone
F,11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Query Local Similarity 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

JN0023

substance P - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: JN0023

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263; PMID:2452461

A:Accession: JN0023

A:Molecule type: protein

A:Residues: 1-11 <CON>

A:Cross-references: UNIPROT:P19850; UNIPARC:UPI0000035243

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

100.0%; Score 21; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 8 FGLM 11

RESULT 4

S33300

probable substance P - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S33300

R:Maughn, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A:Title: Primary structures and biological activities of substance-P-related peptides for

A:Reference number: S33300; MUID:93292508; PMID:7685693

A:Accession: S33300

A:Molecule type: protein

A:Residues: 1-11 <MAN>

A:Cross-references: UNIPROT:P41333; UNIPARC:UPI0000136FDB

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas

A:Note: substance P is derived by post-translational processing of preprotachykinin A

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

100.0%; Score 21; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 8 FGLM 11

RESULT 5

E60409

substance P-like peptide I - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: E60409

R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: E60409

A:Molecule type: protein

A:Residues: 1-11 <SIM>

A:Cross-references: UNIPROT:P42989; UNIPARC:UPI0000136FDB

C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

100.0%; Score 21; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 8 FGLM 11

RESULT 6

F60409

substance P-like peptide II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C:Accession: F60409

R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A:Reference number: A60409; MUID:90287814; PMID:2356157

A:Accession: F60409

A:Molecule type: protein

A:Residues: 1-11 <SIM>

A:Cross-references: UNIPROT:P42990; UNIPARC:UPI0000136FDB

C:Keywords: amidated carboxyl end; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

100.0%; Score 21; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 8 FGLM 11

RESULT 7

S23308

substance P - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004

C:Accession: S23308

R:Jensen, U.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod

A:Reference number: S23308; MUID:92298992; PMID:1376687

A:Accession: S23308

A:Molecule type: protein

A:Residues: 1-11 <JEN>

A:Cross-references: UNIPROT:P28499; UNIPARC:UPI0000035254

A:Experimental source: brain

C:Function:

A:Description: may play a physiological role in the regulation of cardiovascular and gas

A:Note: substance P is derived by post-translational processing of preprotachykinin A

C:Keywords: neuropeptide; amidated carboxyl end; tachykinin

F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

100.0%; Score 21; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 8 FGLM 11

RESULT 8

PS0332

phospholipase A2 (EC 3.1.1.4), sperm - human (fragment)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:17:04 ; Search time 98 Seconds
(without alignments)
28.797 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 34439

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	11	TKN4_PSEGU	P42989 pseudophryn
2	21	100.0	11	TKN5_PSEGU	P42990 pseudophryn
3	21	100.0	11	TKNA_CAYPO	P67932 cavia porce
4	21	100.0	11	TKNA_CHICK	P19850 gallus gall
5	21	100.0	11	TKNA_HORSE	P67933 equus caball
6	21	100.0	11	TKNA_ONCMY	P28499 oncorhynch
7	21	100.0	11	TKNA_SCYCA	P41333 scyllorhynu
8	21	100.0	19	PA25_HUMAN	P24606 homo sapien
9	21	100.0	19	Q9S8E2_SPIOL	Q9S8E2 spiracia ol
10	21	100.0	23	Q4XBUE_PLACH	Q4XBUE plasmodium
11	21	100.0	27	Q4SBA4_TETNG	Q4SBA4 tetradodon n
12	19	90.5	12	PA2B_VIPEO	P1859 vipeira беру
13	19	90.5	28	Q9R4Z1_CHLAU	Q9R4Z1 chloroflexu
14	18	85.7	10	TKN1_SCYCA	P08608 scyllorhynu
15	18	85.7	10	TKNB_RANCA	P22689 rana catesb
16	18	85.7	10	TKS1_AEDAE	P42634 aedes aegypt
17	18	85.7	10	TKS2_AEDAE	P42635 aedes aegypt
18	18	85.7	11	TKN1_UPEIN	P42026 uperoleia i
19	18	85.7	11	TKN1_UPERU	P08612 uperoleia r
20	18	85.7	11	TKN2_UPERU	P08616 uperoleia r
21	18	85.7	11	TKNA_RANCA	P22688 rana catesb
22	18	85.7	11	TKNA_RANCI	P23207 rana ridibu
23	18	85.7	11	TKN1_PHYFU	P08615 physalaemus
24	18	85.7	11	Q9UAR8_AEDAE	Q9UAR8 aedes aegypt
25	18	85.7	15	TKNM_RANMA	Q9UAR8 rana margar
26	18	85.7	15	Q9U0A5_HUMAN	Q9U0A5 homo sapien
27	18	85.7	15	Q9MNO2_PIG	Q9MNO2 sus scrofa
28	18	85.7	17	Q7R8B7_PLAYO	Q7R8B7 plasmodym
29	18	85.7	19	Q31045_STRCO	Q31045 streptomyc
30	18	85.7	20	O61BTS_BOVIN	O61BTS bos taurus
31	18	85.7	21	O61943_MOUSE	O61943 mus musculu

32	18	85.7	25	2	Q80VX3_MOUSE	Q80VX3 mus musculu
33	18	85.7	26	2	Q4TDF2_TETNG	Q4TDF2 tetradodon n
34	18	85.7	28	2	Q58M67_9CAUD	Q58M67 cyanophaga
35	18	85.7	30	2	Q4NMZ2_BACCE	Q4NMZ2 bacillus ce
36	17	81.0	23	2	Q673D7_9CHUR	Q673D7 dehalococco
37	17	81.0	25	2	Q90Z49_HAPBU	Q90Z49 haplochromi
38	17	81.0	26	2	Q99LX4_MOUSE	Q99LX4 mus musculu
39	17	81.0	26	2	Q7LZG4_OXYSC	Q7LZG4 oxyuranus s
40	17	81.0	27	2	Q6LEB1_HUMAN	Q6LEB1 homo sapien
41	17	81.0	27	2	Q8HKH7_9ACAR	Q8HKH7 apnomoma co
42	17	81.0	27	2	Q8HKI3_9ACAR	Q8HKI3 apnomoma co
43	17	81.0	27	2	Q56Z51_ARATH	Q56Z51 arabidopsis
44	17	81.0	27	2	Q7LZG2_OXYSC	Q7LZG2 oxyuranus s
45	17	81.0	28	2	Q673D9_9CHUR	Q673D9 dehalococco

ALIGNMENTS

RESULT 1

ID	TKN4_PSEGU	STANDARD;	PRT;	11 AA.
AC	P42989;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Substance P-like peptide 1 (PG-SP1)			
OS	Pseudophryne guentheri (Guenther's toadlet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;			
OC	Myobatrachinae; Pseudophryne.			
OX	NCBI_TaxID=30349;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RC	TISSUE=Skin secretion;			
RX	MEDLINE=30287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;			
RA	Simmaco M., Severini C., de Blase D., Barra D., Bossa F.,			
RA	Roberts J.D., Melchiorri P., Bräpamer V.;			
RT	"Six novel tachykinin- and bombesin-related peptides from the skin of			
RT	the Australian frog Pseudophryne guentheri.";			
RL	Peptides 11:299-304(1990).			
CC	-1- FUNCTION: Tachykinins are active peptides which excite neurons,			
CC	evoked behavioral responses, are potent vasodilators and			
CC	secretagogues, and contract (directly or indirectly) many smooth			
CC	muscles.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the skin glands.			
CC	-1- SIMILARITY: Belongs to the tachykinin family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	PIR; B60409; B60409.			
DR	InterPro; IPR002040; Tachy Neurokinin.			
DR	InterPro; IPR008215; Tachykinin.			
DR	PIfam; PF02202; Tachykinin; 1.			
DR	SMART; SM00203; TK; 1.			
DR	PROSITE; PS00267; TACHYKININ; 1.			
KW	Amidation; Amphibian defense peptide; Direct protein sequencing;			
KW	Neuropeptide; Pyroglutamate; Pyroglutamate; Pyroglutamate;			
KW	Neuropeptide; Pyroglutamate; Pyroglutamate; Pyroglutamate;			
FT	MOD_RSS 1 11 Methionine amide.			
FT	MOD_RSS 1 11 Methionine amide.			
FT	MOD_RSS 1 11 Methionine amide.			
SQ	SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;			
QY	Query Match 100.0%; Score 21; DB 1; Length 11;			
QY	Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;			
QY	Matches 4; Conservative 0; Mismatches 0;			
QY	1 FGLM 4			
QY				

Db 8 FGLM 11

RESULT 2

TKNS_PSEGU STANDARD; PRT; 11 AA.

ID TKNS_PSEGU

AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Substance P-like peptide II (PC-SPII).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Euxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;

RA Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,

RA Roberts J.D., Melchiorri P., Espamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: F60409; F60409.

DR InterPro: IPR002040; Tachy_Neurokinin.

DR Pfam: PF02202; Tachykinin; 1.

DR PROSITE: PS00267; TACHYKININ; 1.

KW Amidation; Amphibian defense peptide; Direct protein sequencing;

KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.

KW MOD RES 1 1 Pyrrolidone carboxylic acid.

FT MOD RES 11 1 Methionine amide.

FT SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

SQ

Query Match 100.0%; Score 21; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 8 FGLM 11

RESULT 3

TKNA_CAVPO STANDARD; PRT; 11 AA.

ID TKNA_CAVPO

AC P67932; P01290;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Substance P.

GN Name=TRAC1; Synonyms=NKA, NKXA, TAC2;

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

OC Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Small intestine;

RX MEDLINE=90044685; PubMed=2478925; DOI=10.1016/0143-4179(89)90066-8;

RA Murphy R.;

RT "Primary amino acid sequence of guinea-pig substance P.";

RL Neuropeptides 14:105-110(1989).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: A60654; A60654.

DR InterPro: IPR002040; Tachy_Neurokinin.

DR Pfam: PF02202; Tachykinin; 1.

DR PROSITE: PS00267; TACHYKININ; 1.

KW Amidation; Direct protein sequencing; Neuropeptide; Neuropeptide; Tachykinin.

KW MOD RES 11 1 Methionine amide.

FT MOD RES 11 AA; 1349 MW; 3E757FE3C9D6C67 CRC64;

SQ

Query Match 100.0%; Score 21; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

Db 8 FGLM 11

RESULT 4

TKNA_CHICK STANDARD; PRT; 11 AA.

ID TKNA_CHICK

AC P19850;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Substance P.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=90311;

OX [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Intestine.

RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;

RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;

RT "[Arg3]substance P and neurokinin A from chicken small intestine.";

RL Regul. Pept. 20:171-180(1988).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the tachykinin family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR: JN0023; JN0023.

DR InterPro: IPR002040; Tachy_Neurokinin.

DR Pfam: PF02202; Tachykinin; 1.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:06:43 ; Search time 16 Seconds
(without alignments)
20.669 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/backfile1.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1 US-08-441-591-63	Sequence 63, Appl
2	21	100.0	4	1 US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	2 US-09-265-690C-2	Sequence 2, Appl
4	21	100.0	4	2 US-09-635-266-3	Sequence 3, Appl
5	21	100.0	4	2 US-10-230-133-3	Sequence 3, Appl
6	21	100.0	4	2 US-09-623-548A-623	Sequence 623, App
7	21	100.0	4	2 US-10-695-536-3	Sequence 3, Appl
8	21	100.0	4	2 US-09-657-276-623	Sequence 623, App
9	21	100.0	4	4 PCT-US95-05600-80	Sequence 80, Appl
10	21	100.0	5	1 US-07-934-553-2	Sequence 2, Appl
11	21	100.0	5	1 US-08-225-474-2	Sequence 2, Appl
12	21	100.0	5	1 US-08-070-301-6	Sequence 6, Appl
13	21	100.0	5	1 US-07-737-371E-6	Sequence 6, Appl
14	21	100.0	5	1 US-07-737-371E-48	Sequence 48, Appl
15	21	100.0	5	1 US-09-265-690C-1	Sequence 1, Appl
16	21	100.0	5	2 US-09-623-548A-565	Sequence 565, App
17	21	100.0	5	2 US-09-623-548A-604	Sequence 604, App
18	21	100.0	5	2 US-10-134-187-3	Sequence 3, Appl
19	21	100.0	5	2 US-09-657-276-565	Sequence 565, App
20	21	100.0	5	2 US-09-657-276-604	Sequence 604, App
21	21	100.0	6	1 US-07-934-553-3	Sequence 3, Appl
22	21	100.0	6	1 US-08-225-474-3	Sequence 3, Appl
23	21	100.0	6	1 US-08-430-238-15	Sequence 15, Appl
24	21	100.0	6	1 US-07-737-371E-5	Sequence 5, Appl
25	21	100.0	6	1 US-09-317-125-5	Sequence 5, Appl
26	21	100.0	6	2 US-09-428-692-39	Sequence 39, Appl
27	21	100.0	6	2 US-09-428-692-41	Sequence 41, Appl

28	21	100.0	6	2 US-09-623-548A-566	Sequence 566, App
29	21	100.0	6	2 US-09-623-548A-595	Sequence 595, App
30	21	100.0	6	2 US-09-623-548A-597	Sequence 597, App
31	21	100.0	6	2 US-09-623-548A-601	Sequence 601, App
32	21	100.0	6	2 US-09-657-276-566	Sequence 566, App
33	21	100.0	6	2 US-09-657-276-595	Sequence 595, App
34	21	100.0	6	2 US-09-657-276-597	Sequence 597, App
35	21	100.0	6	2 US-09-657-276-601	Sequence 601, App
36	21	100.0	7	1 US-07-712-828B-7	Sequence 7, Appl
37	21	100.0	7	1 US-07-737-371E-8	Sequence 8, Appl
38	21	100.0	7	2 US-09-428-692-42	Sequence 42, Appl
39	21	100.0	7	2 US-09-623-548A-596	Sequence 596, App
40	21	100.0	7	2 US-09-623-548A-607	Sequence 607, App
41	21	100.0	7	2 US-10-134-187-2	Sequence 2, Appl
42	21	100.0	7	2 US-09-657-276-596	Sequence 596, App
43	21	100.0	7	2 US-09-657-276-607	Sequence 607, App
44	21	100.0	8	1 US-07-737-371E-10	Sequence 10, Appl
45	21	100.0	8	1 US-07-737-371E-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-08-441-591-63
Sequence 63, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIDELANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratechun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-63

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 2
US-08-303-362A-63
Sequence 63, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEWLANDT, D., GOLD, L. AND WICKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-303-362A-63

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 3
US-09-265-690C-2
Sequence 2, Application US/09265690C
Patent No. 6372440
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Me
TITLE OF INVENTION: For Disease Diagnosis
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265,690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 4
US-09-635-266-3
Sequence 3, Application US/09635266
Patent No. 6455734
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
TITLE OF INVENTION: methods for treatment of abnormal physiological states
FILE REFERENCE: N1427-002
CURRENT APPLICATION NUMBER: US/09/635,266
CURRENT FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-635-266-3

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:13:24 ; Search time 46 Seconds
(without alignments)
36.333 Million cell updates/sec

Title: US-10-805-881-2

Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	US-09-265-690C-2	Sequence 2, Appli
2	21	100.0	4	US-10-230-133-3	Sequence 3, Appli
3	21	100.0	4	US-10-053-669-2	Sequence 2, Appli
4	21	100.0	4	US-10-695-536-3	Sequence 3, Appli
5	21	100.0	4	US-10-805-881-2	Sequence 2, Appli
6	21	100.0	4	US-10-497-628-2	Sequence 2, Appli
7	21	100.0	4	US-11-018-690-3	Sequence 3, Appli
8	21	100.0	4	US-11-066-697-623	Sequence 623, App
9	21	100.0	5	US-09-265-690C-1	Sequence 1, Appli
10	21	100.0	5	US-10-053-669-1	Sequence 1, Appli
11	21	100.0	5	US-10-134-187-3	Sequence 3, Appli
12	21	100.0	5	US-10-688-741-3	Sequence 3, Appli
13	21	100.0	5	US-10-346-737A-30	Sequence 30, Appli
14	21	100.0	5	US-10-805-881-1	Sequence 1, Appli
15	21	100.0	5	US-10-720-039-3	Sequence 3, Appli
16	21	100.0	5	US-10-497-628-15	Sequence 15, Appli
17	21	100.0	5	US-10-497-628-16	Sequence 16, Appli
18	21	100.0	5	US-10-497-628-17	Sequence 17, Appli
19	21	100.0	5	US-11-066-697-565	Sequence 605, App
20	21	100.0	5	US-11-066-697-604	Sequence 604, App
21	21	100.0	5	US-11-025-494-3	Sequence 3, Appli
22	21	100.0	6	US-10-168-789A-38	Sequence 38, Appli
23	21	100.0	6	US-10-497-628-14	Sequence 14, Appli
24	21	100.0	6	US-10-776-330-4	Sequence 4, Appli
25	21	100.0	6	US-11-066-697-566	Sequence 566, App
26	21	100.0	6	US-11-066-697-595	Sequence 595, App
27	21	100.0	6	US-11-066-697-597	Sequence 597, App

28	21	100.0	6	US-11-066-697-601	Sequence 601, App
29	21	100.0	7	US-10-036-542-110	Sequence 110, App
30	21	100.0	7	US-10-036-542-111	Sequence 111, App
31	21	100.0	7	US-10-168-789A-37	Sequence 37, Appli
32	21	100.0	7	US-10-134-187-2	Sequence 2, Appli
33	21	100.0	7	US-10-688-741-2	Sequence 2, Appli
34	21	100.0	7	US-10-720-039-2	Sequence 13, Appli
35	21	100.0	7	US-10-497-628-13	Sequence 596, App
36	21	100.0	7	US-11-066-697-596	Sequence 607, App
37	21	100.0	7	US-11-025-494-2	Sequence 2, Appli
38	21	100.0	7	US-10-168-789A-36	Sequence 36, Appli
39	21	100.0	8	US-10-497-628-12	Sequence 12, Appli
40	21	100.0	8	US-11-066-697-583	Sequence 583, App
41	21	100.0	8	US-11-066-697-592	Sequence 592, App
42	21	100.0	8	US-11-066-697-600	Sequence 600, App
43	21	100.0	8	US-10-036-542-112	Sequence 112, App
44	21	100.0	9	US-10-168-789A-35	Sequence 35, Appli
45	21	100.0	9	US-10-168-789A-35	Sequence 35, Appli

ALIGNMENTS

```

RESULT 1
US-09-265-690C-2
: Sequence 2, Application US/09265690C
: Publication No. US20010051345A1
: GENERAL INFORMATION:
: APPLICANT: Wells, Ibert
: TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
: FILE REFERENCE: 1427001
: CURRENT APPLICATION NUMBER: US/09/265,690C
: CURRENT FILING DATE: 1999-03-10
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MOD RES
: LOCATION: (4) --(4)
: OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match      100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 FGLM 4
      ||||
Db      1 FGLM 4

RESULT 2
US-10-230-133-3
: Sequence 3, Application US/10230133
: Publication No. US20030040625A1
: GENERAL INFORMATION:
: APPLICANT: Wells, Ibert
: TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
: FILE REFERENCE: 2892-106
: CURRENT APPLICATION NUMBER: US/10/230,133
: CURRENT FILING DATE: 2002-08-29
: PRIOR APPLICATION NUMBER: 09/635,266
: PRIOR FILING DATE: 2000-08-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 4
: TYPE: PRT

```

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FGLM 4
|||
Db 1 FGLM 4

RESULT 3
US-10-053-669-2
Sequence 2, Application US/10053669
Publication No. US2003007658A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
FILE REFERENCE: N1427-005
CURRENT APPLICATION NUMBER: US/10/053,669
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 09/265,690
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-053-669-2

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FGLM 4
|||
Db 1 FGLM 4

RESULT 4
US-10-695-536-3
Sequence 3, Application US/10695536
Publication No. US20040110692A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert Clifton
TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
FILE REFERENCE: 800812-0008
CURRENT APPLICATION NUMBER: US/10/695,536
PRIOR FILING DATE: 2003-10-28
PRIOR APPLICATION NUMBER: US 10/230,133
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 09/635,266
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES

LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-695-536-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FGLM 4
|||
Db 1 FGLM 4

RESULT 5
US-10-805-881-2
Sequence 2, Application US/10805881
Publication No. US20040171093A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert C.
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
FILE REFERENCE: 800812-0005
CURRENT APPLICATION NUMBER: US/10/805,881
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 10/053,669
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 10/695,536
PRIOR FILING DATE: 2003-10-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-805-881-2

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FGLM 4
|||
Db 1 FGLM 4

RESULT 6
US-10-497-628-2
Sequence 2, Application US/10497628
Publication No. US20050009752A1
GENERAL INFORMATION:
APPLICANT: Tetsu Nishida
APPLICANT: Makoto Inui
TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
FILE REFERENCE: 04355/HG
CURRENT APPLICATION NUMBER: US/10/497,628
PRIOR FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: JP 2001-368103
PRIOR FILING DATE: 2001-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Human
US-10-497-628-2

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:09:53 : Search time 2.85714 Seconds
(without alignments)
4.243 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 7285

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 100%

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	76.2	8	US-11-044-051-80	Sequence 80, Appl
2	16	76.2	9	US-11-044-051-78	Sequence 78, Appl
3	16	76.2	9	US-11-044-051-79	Sequence 79, Appl
4	16	76.2	10	US-11-044-051-77	Sequence 77, Appl
5	16	76.2	10	US-11-044-051-85	Sequence 85, Appl
6	16	76.2	10	US-11-044-051-87	Sequence 87, Appl
7	16	76.2	10	US-11-044-051-88	Sequence 88, Appl
8	16	76.2	13	US-10-986-501-361	Sequence 361, App
9	16	76.2	16	US-11-044-051-81	Sequence 81, Appl
10	16	76.2	19	US-10-503-575-149	Sequence 149, App
11	16	76.2	19	US-11-054-515-2170	Sequence 2170, App
12	15	71.4	8	US-11-054-515-3132	Sequence 3132, Ap
13	15	71.4	12	US-10-923-605-4	Sequence 4, Appli
14	15	71.4	12	US-10-934-818-4	Sequence 478, App
15	15	71.4	13	US-10-511-559-478	Sequence 479, App
16	15	71.4	13	US-10-511-559-479	Sequence 480, App
17	15	71.4	13	US-10-511-559-480	Sequence 481, App
18	15	71.4	13	US-10-511-559-481	Sequence 482, App
19	15	71.4	13	US-10-511-559-482	Sequence 293, App
20	15	71.4	13	US-11-054-515-2943	Sequence 259, App
21	15	71.4	19	US-10-503-575-259	Sequence 177, App
22	15	71.4	28	US-11-021-441-50	Sequence 10, Appl
23	15	71.4	30	US-11-033-498-10	Sequence 82, Appl
24	14	66.7	10	US-11-044-051-82	
25	14	66.7	10	US-11-044-051-82	

26	14	66.7	10	7	US-11-044-051-83	Sequence 83, Appl
27	14	66.7	10	7	US-11-044-051-84	Sequence 84, Appl
28	14	66.7	10	7	US-11-044-051-86	Sequence 86, Appl
29	14	66.7	13	7	US-11-054-515-2777	Sequence 2777, Ap
30	14	66.7	15	7	US-11-054-515-2976	Sequence 2976, Ap
31	14	66.7	16	7	US-11-054-515-3004	Sequence 3004, Ap
32	14	66.7	16	7	US-11-054-515-3071	Sequence 3071, Ap
33	14	66.7	17	7	US-11-054-515-2929	Sequence 2929, Ap
34	14	66.7	18	7	US-11-119-581-53	Sequence 53, Appl
35	14	66.7	18	7	US-11-054-515-3136	Sequence 3136, Ap
36	14	66.7	26	1	US-10-939-890-484	Sequence 484, App
37	13	61.9	7	1	US-10-494-781-21	Sequence 21, Appli
38	13	61.9	9	7	US-11-053-100-9	Sequence 9, Appli
39	13	61.9	9	7	US-11-054-515-2178	Sequence 2178, Ap
40	13	61.9	10	7	US-11-152-747-40	Sequence 40, Appl
41	13	61.9	10	7	US-11-054-515-2957	Sequence 2957, Ap
42	13	61.9	12	1	US-10-983-664-18	Sequence 18, Appl
43	13	61.9	12	1	US-11-054-515-3176	Sequence 3176, Ap
44	13	61.9	14	1	US-10-939-890-86	Sequence 86, Appl
45	13	61.9	14	7	US-11-054-515-2462	Sequence 2462, Ap

ALIGNMENTS

```

RESULT 1
US-11-044-051-80
; Sequence 80, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: CODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-PALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044, 051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459, 263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-80

Query Match      76.2%; Score 16; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 FGL 3
      |||
Db      3 FGL 5

RESULT 2
US-11-044-051-78
; Sequence 78, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: CODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-PALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044, 051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459, 263

```

; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-78

Query Match 76.2%; Score 16; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
|||
Db 2 FGL 4

RESULT 3
US-11-044-051-79
; Sequence 79, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 79
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-79

Query Match 76.2%; Score 16; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
|||
Db 3 FGL 5

RESULT 4
US-11-044-051-77
; Sequence 77, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 77
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-044-051-77

Query Match 76.2%; Score 16; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
|||
Db 3 FGL 5

RESULT 5
US-11-044-051-85
; Sequence 85, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-85

Query Match 76.2%; Score 16; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3
|||
Db 3 FGL 5

RESULT 6
US-11-044-051-87
; Sequence 87, Application US/11044051
; Publication No. US20050255553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 87
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-87

Query Match 76.2%; Score 16; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:18:39 ; Search time 182 Seconds
(without alignments)
9.657 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 25265

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	2 AAW41683	AAW41683 Peptide u
2	21	100.0	4	2 AAY31075	AAY31075 Non-cross
3	21	100.0	4	3 AAB23026	AAB23026 Human/rat
4	21	100.0	4	3 AAY67577	AAY67577 P antagon
5	21	100.0	4	4 AAB91447	AAB91447 Tachykini
6	21	100.0	4	5 ABB10091	ABB10091 Substance
7	21	100.0	4	5 AAU77846	AAU77846 Tachykini
8	21	100.0	4	7 ADE94198	ADE94198 High acti
9	21	100.0	4	8 ADR43772	ADR43772 Human mag
10	18	85.7	4	1 AAP61654	AAP61654 Sequence
11	18	85.7	4	1 AAP71301	AAP71301 Peptide c
12	18	85.7	4	2 AAW41686	AAW41686 Tetrarept
13	18	85.7	4	5 ABB10092	ABB10092 Substance
14	18	85.7	4	5 AAB61707	AAB61707 Sequence
15	16	76.2	4	1 AAP71312	AAP71312 Peptide c
16	16	76.2	4	2 AAY23485	AAY23485 V beta 6
17	16	76.2	4	3 AAB12293	AAB12293 Prolong o
18	16	76.2	4	4 AAG62647	AAG62647 Typical c
19	16	76.2	4	5 ABB88046	ABB88046 Enzyme cl
20	16	76.2	4	8 ADL78809	ADL78809 Exemplary
21	16	76.2	4	9 ADY04142	ADY04142 Peptide d
22	15	71.4	3	3 AAY67578	AAY67578 P antagon
23	15	71.4	3	4 AAB91448	AAB91448 Tachykini
24	15	71.4	4	1 AAP60334	AAP60334 Peptide w

25	15	71.4	4	2 AAW77469	AAW77469 Tetrarept
26	15	71.4	4	2 AAW41684	AAW41684 Tetrarept
27	15	71.4	4	2 AAW41685	AAW41685 Tetrarept
28	15	71.4	4	4 AAB91795	AAB91795 Amyloid b
29	15	71.4	4	4 AAB91822	AAB91822 Amyloid b
30	14	66.7	4	1 AAP61659	AAP61659 Sequence
31	14	66.7	4	1 AAP71306	AAP71306 Peptide c
32	14	66.7	4	2 AAB34486	AAB34486 FGIA. 8/1
33	14	66.7	4	2 AAR46020	AAR46020 Serine pr
34	14	66.7	4	2 AAR93149	AAR93149 Mycobacte
35	14	66.7	4	3 AAB12292	AAB12292 Prolong o
36	14	66.7	4	4 AAB91714	AAB91714 Opioid pe
37	14	66.7	4	5 ABB88045	ABB88045 Enzyme c1
38	14	66.7	4	5 ABB32223	ABB32223 Sheep col
39	14	66.7	4	8 ADQ91509	ADQ91509 HIV trunc
40	14	66.7	4	8 ADS74433	ADS74433 Ovine col
41	13	61.9	3	5 ABG77484	ABG77484 Targettin
42	13	61.9	4	1 AAP61658	AAP61658 Sequence
43	13	61.9	4	1 AAP71287	AAP71287 Opiate bi
44	13	61.9	4	1 AAP82691	AAP82691 Renin inh
45	13	61.9	4	2 AAR15768	AAR15768 Farnesyl-

ALIGNMENTS

RESULT 1	AAW41683	AAW41683 standard; peptide; 4 AA.
ID	AAW41683	AAW41683 standard; peptide; 4 AA.
AC	AAW41683;	
DT	09-JUN-1998	(first entry)
DE	Peptide used in ophthalmic drug to treat corneal disorders.	
XX	Optthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;	
KW	keratitis; insulin like growth factor-I; IGF-I; eye drop.	
OS	Synthetic.	
XX		
FM	Key	Location/Qualifiers
FT	Modified-site	4
XX		/note= "C-terminal amide"
XX	W09749419-A1.	
XX	31-DEC-1997.	
XX	11-JUN-1997;	97MO-JP002015.
XX	26-JUN-1996;	96UP-00165612.
PA	(SANT) SANTEN PHARM CO LTD.	
XX		
PI	Nishida T, Nakamura M, Nakata K;	
XX	WPI, 1998-076907/07.	
DR		
XX		
PT	Optthalmic drug composition containing tetra:peptide - is useful as	
PT	corneal disorder remedy for corneal ulcer, corneal epithelial peeling,	
PT	dry eye, keratitis.	
PS	Claim 1, Page 15; 19pp; Japanese.	
XX		
CC	The present sequence represents a tetrapeptide which is the active	
CC	ingredient in an ophthalmic drug composition. It is used, together with	
CC	insulin like growth factor-I (IGF-I), to treat corneal disorders such as	
CC	corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The	
CC	dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and	
CC	0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of	
CC	the composition is eye drops	
XX		

SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
 1 FGLM 4

RESULT 2
 AAY31075
 ID AAY31075 standard; peptide; 4 AA.

AC AAY31075;

DT 21-OCT-1999 (first entry)

DE Non-crosslinked protein particle peptide 124.

XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KM albumin; haemoglobin; nanometer; micrometer; clearance.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 4 /note= "C-terminal amide"

PN US5945033-A.

PD 31-AUG-1999.

PF 12-NOV-1996; 96US-00747137.

PR 15-JAN-1991; 91US-00641720.

PR 13-OCT-1992; 92US-00959560.

PR 01-JUN-1993; 93US-00069831.

PR 14-MAR-1994; 94US-00212546.

PA (HEMO-) HEMOSPHERE INC.

XX Yen RCK;

PI WPI; 1999-508153/42.

DR WPI; 1999-508153/42.

XX Non-crosslinked protein particles for therapeutic and diagnostic use.

PT Example 22; Col 103-104; 65pp; English.

PS This invention describes a novel aqueous suspension of monodisperse

XX particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is

CC stable against dissolving upon dilution with an alcohol-free aqueous

CC medium. The method involves (a) forming an aqueous solution containing

CC albumin and hemoglobin and (b) treating the aqueous solution with an

CC alcohol to cause the solution to become turbid. The particles are useful

CC as agents for in vivo administration, either of their own administration

CC or as a vehicle for other therapeutic or diagnostic agents. The method

CC permits the formation of albumin and hemoglobin particles in the

CC nanometer and micrometer size range, in a form closer to their natural

CC form than the forms of the prior art. The particles therefore constitute

CC a more closely controlled agent for in vivo administration, with greater

CC ease of clearance from the body after their period of usefulness.

CC AAY30952-Y3115 represent peptides used in the method of the invention

XX Sequence 4 AA;

SQ Query Match 100.0%; Score 21; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FGLM 4
 1 FGLM 4

RESULT 3
 AAB23026
 ID AAB23026 standard; peptide; 4 AA.

AC AAB23026;

DT 16-JAN-2001 (first entry)

DE Human/rat tachykinin Substance P C-terminal tetrapeptide.

XX Substance P; tachykinin; human; rat; magnesium binding defect;
 KM sodium sensitive essential hypertension; insulin resistance;
 KW type 2 diabetes; antibody; immunoassay; quantification.

XX Homo sapiens.

OS Rattus sp.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"

PN W0200054053-A1.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US003707.

PR 10-MAR-1999; 99US-00265690.

PA (WELL/) WELLS I C.

PI Wells IC;

DR WPI; 2000-587457/55.

XX Detecting magnesium binding defects associated with abnormal

PT physiological states such as sodium-sensitive essential hypertension and
 PT type 2 insulin-resistant diabetes mellitus, comprises measuring a
 PT specific pentapeptide in blood.

XX Disclosure; Page 5; 21pp; English.

PS The invention relates to a method for detecting magnesium binding

CC defects. The method comprises quantitating a tachykinin C-terminal

CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,

CC AAB23026) in blood using an antibody specific for the generalised

CC mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-

CC NH₂ (AAB23028). The method is useful for detecting cellular states

CC such as sodium-sensitive essential hypertension and type 2 diabetes

CC mellitus. The present sequence represents the C-terminal 4 amino acids of

CC the tachykinin Substance P (AAB23027) from human and rat. This is a

CC degradation product of the Substance P C-terminal pentapeptide (AAB23025)

CC and may also be assayed according to the method of the invention

XX Sequence 4 AA;

SQ Query Match 100.0%; Score 21; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
 1 FGLM 4

RESULT 4
 AAY67577
 ID AAY67577 standard; peptide; 4 AA.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:28:09 ; Search time 38 Seconds
(without alignments)
10.128 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	47.6	4	2	PT0240 Ig heavy chain CRD
2	10	47.6	4	2	A53284 T-cell receptor be
3	8	38.1	4	2	PT0633 T-cell receptor be
4	7	33.3	3	3	B23751 spinal cord peptid
5	7	33.3	4	2	E44823 synaposomal-assoc
6	7	33.3	4	2	B53284 T-cell receptor be
7	6	28.6	3	3	PT0636 T-cell receptor be
8	6	28.6	3	3	PT0571 T-cell receptor be
9	6	28.6	3	3	S68328 blood cell protein
10	6	28.6	3	3	GKHU growth-modulating
11	6	28.6	3	3	A60898 bursin - chicken
12	6	28.6	3	3	A23751 spinal cord peptid
13	6	28.6	4	1	ECXAA antio-Rfamide neur
14	6	28.6	4	2	D41654 hypothetical prote
15	6	28.6	4	2	S53508 starvation-induced
16	6	28.6	4	2	T30569 hypothetrical prote
17	6	28.6	4	2	I38888 COI inttron 16 prot
18	6	28.6	4	2	A25844 antio-RF amide neu
19	6	28.6	4	2	A34626 RPHH-related neuro
20	6	28.6	4	2	S59390 wposin-light-chain
21	6	28.6	4	2	S43959 Ig mu chain V regi
22	6	28.6	4	2	S47552 ubiquitin - rat
23	6	28.6	4	2	S09478 carbon-monoxide de
24	6	28.6	4	2	PU0140 globulin IV alpha
25	6	28.6	4	2	J01273 neuropeptide Antio
26	6	28.6	4	2	A35779 neuropeptide Antio
27	6	28.6	4	2	A60418 FMRFamide - polych
28	6	28.6	4	2	A32480 achnatin-I - giant
29	6	28.6	4	2	PT0271 Ig heavy chain CRD

30	6	28.6	4	2	PT0711 T-cell receptor be
31	6	28.6	4	2	PT0698 T-cell receptor be
32	6	28.6	4	2	PT0677 T-cell receptor be
33	6	28.6	4	2	PT0706 T-cell receptor be
34	6	28.6	4	2	PT0675 T-cell receptor be
35	6	28.6	4	2	PT0721 T-cell receptor be
36	6	28.6	4	2	PT0566 T-cell receptor be
37	6	28.6	4	2	ECNK cardioexcitatory n
38	6	28.6	4	2	A32039 tyrosine-melanocyt
39	6	23.8	3	3	PQ0010 angiotensin-conver
40	5	23.8	3	3	S13894 histidinol dehydro
41	5	23.8	3	3	I50412 gene p20K protein
42	5	23.8	3	3	PT0578 T-cell receptor be
43	5	23.8	3	3	I78890 tyrosine protein k
44	5	23.8	3	3	T13892 cytochrome-c oxid
45	5	23.8	4	2	S18401 thyroglobulin - do

ALIGNMENTS

RESULT 1
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; PMID:91108337; PMID:1899102
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Cross-references: UNIPARC:UPI000017C1E2
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Oy 2 GL 3
Db 3 GL 4

RESULT 2

A53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germ-line diversity and j
A:Reference number: A53284; PMID:91342695; PMID:1678859
A:Accession: A53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: UNIPARC:UPI000011E8F2; GB:S60737; NID:G233916; PIDN:AB19517.1; PID:
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60739)
C:Keywords: T-cell receptor

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Oy 2 GL 3
Db 1 GL 2

RESULT 3

PT0633
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: PT0633
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0633
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-4 <FEB>
A/Cross-references: UNIPROT:08BIV7; UNIPARC:UPI000017C7DF
A/Experimental source: newborn thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 38.1%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 G 3
|
Db 3 G 4

RESULT 4

B23751
spinal cord peptide SCP-5 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C/Accession: B23751
R/Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A/Reference number: A23751; MUID:85250425; PMID:4015098
A/Accession: B23751
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-3 <HSI>
A/Cross-references: UNIPARC:UPI000017CE98

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LM 4
|
Db 1 MM 2

RESULT 5

E44823
synaposomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N/Alternate names: superprotein peptide 1
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C/Accession: E44823
R/Loewy, A.; Liu, W.S.; Baltinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: A44823; MUID:92044785; PMID:1941090
A/Accession: E44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-4 <LOB>
A/Cross-references: UNIPARC:UPI000017C5E3
A/Experimental source: visual tissue
A/Note: sequence extracted from NCBI backbone (NCBIPI:64247)
C/Keywords: membrane trafficking

Query Match 33.3%; Score 7; DB 2; Length 4;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LM 4
|
Db 1 IM 2

RESULT 6

B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C/Accession: B53284
R/Haridranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and J
A/Reference number: A53284; MUID:91342695; PMID:1678859
A/Accession: B53284
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-4 <HAR>
A/Cross-references: UNIPARC:UPI000011BEF3; GB:S60737; MUID:9233916; PTDN:AA19518.1; PID:
A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60738)
C/Keywords: T-cell receptor

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FG 2
|
Db 2 WG 3

RESULT 7

PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: PT0636
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0636
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-3 <FEB>
A/Cross-references: UNIPARC:UPI000017CE9E
A/Experimental source: newborn thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 28.6%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 G 2
|
Db 3 G 3

RESULT 8

PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: PT0571
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0571

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:27:59 ; Search time 225 Seconds
(without alignments)
12.543 Million cell updates/sec

Title: US-10-805-881-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	57.1	4	1	OCPL OCTMI
2	9	42.9	4	1	ILME SEPOF
3	6	28.6	2	1	GMA SEPOF
4	6	28.6	3	1	GRM_HUMAN
5	6	28.6	4	1	ACH1_ACHFU
6	6	28.6	4	1	DCML_PSECH
7	6	28.6	4	1	EOS1_HUMAN
8	6	28.6	4	1	PAR3_HIRME
9	6	28.6	4	1	PAR4_HIRME
10	6	28.6	4	1	FRKA_ANTEL
11	6	28.6	4	1	FLRF_HELTI
12	6	28.6	4	1	FLRF_HIRME
13	6	28.6	4	1	FLRN_ANTEL
14	6	28.6	4	1	FMRF_HELTI
15	6	28.6	4	1	FMRF_HIRME
16	6	28.6	4	1	FMRF_MACNI
17	6	28.6	4	1	FMRF_NERYI
18	6	28.6	4	1	OCPL OCTMI
19	6	28.6	4	1	OCPL OCTMI
20	6	28.6	4	1	TPANI PANIM
21	6	28.6	4	2	Q16047_HUMAN
22	5	23.8	4	2	DCMS_PSECH
23	5	23.8	4	2	Q96AT0_HUMAN
24	4	19.0	4	2	TPAN2 PANIM
25	4	19.0	4	2	Q08433_9MURI
26	2	9.5	3	1	LUXE_VIBRI
27	1	4.8	4	1	YIM1_YEAST
28	0	0.0	3	1	THYL_BOMOR
29	0	0.0	3	1	THYL_NOTVI
30	0	0.0	3	1	THYL_PIG
31	0	0.0	3	1	THYL_SHEEP

32 0 0.0 4 1 TUFT_HUMAN P01858 homo sapien
ALIGNMENTS

```
RESULT 1
OCPL OCTMI STANDARD; PRT; 4 AA.
AC P56648.28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardiac active peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardiac active peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardiac active; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MM=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC D-amino acid; Direct protein sequencing; Hormone.
KM MOD_RES 2 D-phenylalanine (in form Ocp-1).
FT SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
SQ
Query Match 57.1%; Score 12; DB 1; Length 4;
Best local similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FG 2
Db 2 FG 3
RESULT 2
ILME SEPOF STANDARD; PRT; 4 AA.
ID AC P83568.29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
CC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=EGG;
RX MEDLINE=2403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis.";
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
```

```

RN [2]
RP PROTEIN SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)00366-3;
RA Zakyiny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
  attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -1- FUNCTION: Has myotropic activity targeting the genital tract.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).
CC -1- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Direct protein sequencing; Pheromone.
KM SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;
SQ
Query Match 42.9%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LM 4
DB 2 LM 3

RESULT 3
GWA_SEPOP STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxId=6610;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Tip-amide-related
  peptide inhibiting the motility of the mature oviduct in the
  cuttlefish, Sepia officinalis.";
RL Peptides 16:1469-1474(1997).
CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity
  targeting the distal oviduct. Inhibits the motility of the oviduct
  by decreasing tonus, frequency and amplitude of contractions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Direct protein sequencing; Neuropeptide.
KM MOD_RES 2 Tryptophan amide.
FT MOD_RES 2 Tryptophan amide.
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2
DB 2 G 2

```

```

DB 1 G 1

RESULT 4
GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycy1-histidyl-lysine.";
RL Experientia 33:324-325(1977)
CC -1- MISCELLANEOUS: This serum tripeptide has been found to stimulate
  growth of some cell types and to inhibit other types in vitro.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC GO: GO:0001558; P:regulation of cell growth; NAS.
KM Direct protein sequencing.
SQ SEQUENCE 3 AA; 340 MW; 6331B81000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2
DB 1 G 1

RESULT 5
ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigurethra; Achatinidae; Achatinidae; Achatina.
OX NCBI_TaxId=6530;
RN [1]
RP PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Feurusac; TISSUE=Ganglion;
RX MEDLINE=89273511; PubMed=2597281;
RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
  fulica Feurusac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Feurusac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneka Y., Kobayashi M.;

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:31:00 ; Search time 45 Seconds
(without alignments)
7.349 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 13782

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	1	US-08-441-591-63 Sequence 63, Appl
2	21	100.0	4	1	US-08-303-362A-63 Sequence 63, Appl
3	21	100.0	4	2	US-09-265-690C-2 Sequence 2, Appli
4	21	100.0	4	2	US-09-635-266-3 Sequence 3, Appli
5	21	100.0	4	2	US-10-230-133-3 Sequence 3, Appli
6	21	100.0	4	2	US-09-623-548A-623 Sequence 623, App
7	21	100.0	4	2	US-10-695-536-3 Sequence 3, Appli
8	21	100.0	4	2	US-09-657-276-623 Sequence 623, App
9	21	100.0	4	4	PCT-US95-05600-80 Sequence 80, Appl
10	16	76.2	4	1	US-08-747-137-124 Sequence 124, App
11	16	76.2	4	2	US-08-722-126A-20 Sequence 20, Appl
12	15	71.4	3	2	US-09-635-266-2 Sequence 2, Appli
13	15	71.4	3	2	US-10-230-133-2 Sequence 2, Appli
14	15	71.4	3	2	US-09-623-548A-624 Sequence 624, App
15	15	71.4	3	2	US-10-695-536-2 Sequence 2, Appli
16	15	71.4	3	2	US-09-657-276-624 Sequence 624, App
17	15	71.4	4	1	US-08-070-301-8 Sequence 8, Appli
18	15	71.4	4	1	US-08-433-401-4 Sequence 4, Appli
19	15	71.4	4	2	US-09-623-548A-971 Sequence 971, App
20	15	71.4	4	2	US-09-623-548A-998 Sequence 998, App
21	15	71.4	4	2	US-09-657-276-971 Sequence 971, App
22	15	71.4	4	2	US-09-657-276-998 Sequence 998, App
23	14	66.7	4	2	US-08-793-701-25 Sequence 25, Appl
24	14	66.7	4	2	US-09-579-264-25 Sequence 25, Appl
25	14	66.7	4	2	US-09-623-548A-890 Sequence 890, App
26	14	66.7	4	2	US-09-657-276-890 Sequence 890, App
27	13	61.9	4	1	US-08-429-964-37 Sequence 37, Appl

28	13	61.9	4	2	US-08-812-586-60 Sequence 60, Appl
29	13	61.9	4	2	US-08-669-656A-11 Sequence 11, Appl
30	13	61.9	4	2	US-09-535-832A-56 Sequence 56, Appl
31	13	61.9	4	2	US-09-665-362A-31 Sequence 31, Appl
32	13	61.9	4	2	US-09-665-637-31 Sequence 31, Appl
33	13	61.9	4	2	US-10-087-402-10 Sequence 10, Appl
34	13	61.9	4	2	US-10-083-894-31 Sequence 31, Appl
35	13	61.9	4	4	PCT-US93-08062-37 Sequence 37, Appl
36	12	57.1	3	1	US-08-343-943-4 Sequence 4, Appli
37	12	57.1	3	1	US-09-060-455-2 Sequence 2, Appli
38	12	57.1	3	2	US-09-150-621-3 Sequence 3, Appli
39	12	57.1	3	2	US-10-121-857-6 Sequence 6, Appli
40	12	57.1	3	2	US-09-623-548A-1527 Sequence 1527, Ap
41	12	57.1	3	2	US-09-657-276-1527 Sequence 1527, Ap
42	12	57.1	3	2	US-10-104-307-3 Sequence 3, Appli
43	12	57.1	4	1	US-07-657-769B-58 Sequence 58, Appl
44	12	57.1	4	1	US-07-822-924-3 Sequence 3, Appli
45	12	57.1	4	1	US-07-822-924-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-441-591-63
Sequence 63, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-63

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
1 1111
Db 1 FGLM 4

RESULT 2
US-08-303-362A-63
Sequence 63, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WICKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: BARRY J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-303-362A-63

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
1 1111
Db 1 FGLM 4

RESULT 3
US-09-265-690C-2
Sequence 2, Application US/09265690C
Patent No. 6372440
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265,690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
1 1111
Db 1 FGLM 4

RESULT 4
US-09-635-266-3
Sequence 3, Application US/09635266
Patent No. 6455714
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
FILE REFERENCE: N1427-002
CURRENT APPLICATION NUMBER: US/09/635,266
CURRENT FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-09-635-266-3

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
1 1111
Db 1 FGLM 4

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:38:10 ; Search time 159 Seconds
(without alignments)
10.511 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 13481

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:*
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	US-09-265-690C-2	Sequence 2, Appli
2	21	100.0	4	US-10-230-133-3	Sequence 3, Appli
3	21	100.0	4	US-10-053-669-2	Sequence 2, Appli
4	21	100.0	4	US-10-695-536-3	Sequence 3, Appli
5	21	100.0	4	US-10-805-881-2	Sequence 2, Appli
6	21	100.0	4	US-10-497-628-2	Sequence 2, Appli
7	21	100.0	4	US-11-018-690-3	Sequence 3, Appli
8	21	100.0	4	US-11-066-697-623	Sequence 623, App
9	16	76.2	4	US-09-879-442A-9	Sequence 9, Appli
10	16	76.2	4	US-10-821-240A-270	Sequence 270, App
11	15	71.4	3	US-10-230-133-2	Sequence 2, Appli
12	15	71.4	3	US-10-695-536-2	Sequence 2, Appli
13	15	71.4	3	US-11-018-690-2	Sequence 2, Appli
14	15	71.4	3	US-11-066-697-624	Sequence 624, App
15	15	71.4	4	US-11-066-697-971	Sequence 971, App
16	15	71.4	4	US-11-066-697-998	Sequence 998, App
17	14	66.7	4	US-09-879-442A-8	Sequence 8, Appli
18	14	66.7	4	US-10-117-867-328	Sequence 328, App
19	14	66.7	4	US-10-433-709-17	Sequence 17, Appli
20	14	66.7	4	US-11-066-697-890	Sequence 890, App
21	13	61.9	4	US-09-879-442A-98	Sequence 98, Appli
22	13	61.9	4	US-09-879-442A-99	Sequence 99, Appli
23	13	61.9	4	US-09-943-123-24	Sequence 24, Appli
24	13	61.9	4	US-10-087-905-30	Sequence 30, Appli
25	13	61.9	4	US-10-087-942-30	Sequence 30, Appli
26	13	61.9	4	US-10-087-402-10	Sequence 10, Appli
27	13	61.9	4	US-10-083-894-31	Sequence 31, Appli

28	13	61.9	4	US-10-196-394-98	Sequence 98, Appli
29	13	61.9	4	US-10-202-824-11	Sequence 11, Appli
30	13	61.9	4	US-10-359-363A-104	Sequence 104, App
31	13	61.9	4	US-10-491-418-21	Sequence 21, Appli
32	13	61.9	4	US-10-712-359A-24	Sequence 24, Appli
33	13	61.9	4	US-10-476-861A-11	Sequence 11, Appli
34	13	61.9	4	US-10-476-861A-118	Sequence 118, App
35	13	61.9	4	US-11-136-464-11	Sequence 11, Appli
36	12	57.1	3	US-10-121-857-6	Sequence 6, Appli
37	12	57.1	3	US-10-255-679-3	Sequence 3, Appli
38	12	57.1	3	US-10-208-018-6	Sequence 6, Appli
39	12	57.1	3	US-10-104-307-3	Sequence 3, Appli
40	12	57.1	3	US-11-066-697-1527	Sequence 1527, Ap
41	12	57.1	4	US-08-484-409-14	Sequence 14, Appli
42	12	57.1	4	US-08-484-409-25	Sequence 25, Appli
43	12	57.1	4	US-09-804-733A-24	Sequence 24, Appli
44	12	57.1	4	US-09-803-126-20	Sequence 20, Appli
45	12	57.1	4	US-09-726-470A-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-09-265-690C-2
Sequence 2, Application US/09265690C
Publication No. US20010051345A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265,690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (4) ..(4)
OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGLM 4
DB 1 FGLM 4
RESULT 2
US-10-230-133-3
Sequence 3, Application US/10230133
Publication No. US20030040625A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
FILE REFERENCE: 2892-106
CURRENT APPLICATION NUMBER: US/10/230,133
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 09/635,266
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 4
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 1 FGLM 4

RESULT 3
US-10-053-669-2
Sequence 2, Application US/10053669
Publication No. US2003007658A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
FILE REFERENCE: N1427-005
CURRENT APPLICATION NUMBER: US/10/053,669
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 09/265,690
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-053-669-2

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 1 FGLM 4

RESULT 4
US-10-695-536-3
Sequence 3, Application US/10695536
Publication No. US20040110692A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert Clifton
TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
FILE REFERENCE: 800812-0008
CURRENT APPLICATION NUMBER: US/10/695,536
PRIOR FILING DATE: 2003-10-28
PRIOR APPLICATION NUMBER: US 10/230,133
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 09/635,266
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES

LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-695-536-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 1 FGLM 4

RESULT 5
US-10-805-881-2
Sequence 2, Application US/10805881
Publication No. US20040171093A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert C.
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
FILE REFERENCE: 800812-0005
CURRENT APPLICATION NUMBER: US/10/805,881
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 10/053,669
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 10/695,536
PRIOR FILING DATE: 2003-10-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: AMIDATION
US-10-805-881-2

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db 1 FGLM 4

RESULT 6
US-10-497-628-2
Sequence 2, Application US/10497628
Publication No. US2005009752A1
GENERAL INFORMATION:
APPLICANT: Tenu Nishida
APPLICANT: Makoto Inui
TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
FILE REFERENCE: 04355/HG
CURRENT APPLICATION NUMBER: US/10/497,628
PRIOR FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: JP 2001-368103
PRIOR FILING DATE: 2001-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Human
US-10-497-628-2

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 02:38:51 ; Search time 8 Seconds
(without alignments)
1.515 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 94

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	47.6	4	US-11-046-456-27	Sequence 27, Appl
2	10	47.6	4	US-11-046-644-27	Sequence 27, Appl
3	10	47.6	4	US-11-052-168A-38	Sequence 38, Appl
4	8	38.1	4	US-11-064-785-1	Sequence 1, Appl
5	7	33.3	4	US-10-977-367-21	Sequence 21, Appl
6	7	33.3	4	US-10-977-367-36	Sequence 36, Appl
7	7	33.3	4	US-10-997-066-16	Sequence 16, Appl
8	7	33.3	4	US-11-035-682-12	Sequence 12, Appl
9	6	28.6	3	US-11-052-168A-4	Sequence 4, Appl
10	6	28.6	3	US-11-052-168A-39	Sequence 39, Appl
11	6	28.6	4	US-10-503-575-48	Sequence 48, Appl
12	6	28.6	4	US-10-503-575-49	Sequence 49, Appl
13	6	28.6	4	US-10-503-575-59	Sequence 59, Appl
14	6	28.6	4	US-10-503-575-62	Sequence 62, Appl
15	6	28.6	4	US-10-977-367-1	Sequence 1, Appl
16	6	28.6	4	US-10-979-821-77	Sequence 77, Appl
17	6	28.6	4	US-10-939-890-18	Sequence 18, Appl
18	6	28.6	4	US-10-939-890-262	Sequence 262, App
19	6	28.6	4	US-10-939-890-791	Sequence 791, App
20	6	28.6	4	US-10-939-890-792	Sequence 792, App
21	6	28.6	4	US-10-939-890-871	Sequence 871, App
22	6	28.6	4	US-10-966-648-28	Sequence 28, Appl
23	6	28.6	4	US-10-484-271A-7	Sequence 7, Appl
24	6	28.6	4	US-10-516-768-38	Sequence 38, Appl
25	6	28.6	4	US-10-997-759-57	Sequence 57, Appl

26	6	28.6	4	US-11-016-503-26	Sequence 26, Appl
27	6	28.6	4	US-11-176-868-27	Sequence 27, Appl
28	6	28.6	4	US-11-176-868-36	Sequence 36, Appl
29	6	28.6	4	US-11-176-868-39	Sequence 39, Appl
30	6	28.6	4	US-11-010-954-27	Sequence 27, Appl
31	6	28.6	4	US-11-022-289-15	Sequence 15, Appl
32	6	28.6	4	US-11-033-365-53	Sequence 53, Appl
33	6	28.6	4	US-11-052-168A-2	Sequence 2, Appl
34	6	28.6	4	US-11-053-100-1	Sequence 1, Appl
35	6	28.6	4	US-11-053-100-2	Sequence 2, Appl
36	6	28.6	4	US-11-053-750-27	Sequence 27, Appl
37	6	28.6	4	US-11-113-224-57	Sequence 57, Appl
38	6	28.6	4	US-11-113-224-59	Sequence 59, Appl
39	5	23.8	4	US-10-845-413-154	Sequence 154, App
40	4	19.0	4	US-10-503-575-61	Sequence 61, Appl
41	4	19.0	4	US-10-444-662-3	Sequence 3, Appl
42	4	19.0	4	US-10-667-295-262	Sequence 262, App
43	4	19.0	4	US-10-667-295-263	Sequence 263, App
44	4	19.0	4	US-11-011-666-14	Sequence 14, Appl
45	4	19.0	4	US-11-016-503-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-11-046-456-27
Sequence 27, Application US/11046456
Publication No. US20050256044A1
GENERAL INFORMATION:
APPLICANT: Boyle, Bryan
APPLICANT: Funk, Walter
APPLICANT: Kakitani, Makoto
APPLICANT: Oshima, Takeshi
APPLICANT: Park, Eun Ju
APPLICANT: Tang, Y. Tom
APPLICANT: Yeag, Mikio
APPLICANT: Tomizuka, Kazuma
TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
FILE REFERENCE: 18824-003001
CURRENT APPLICATION NUMBER: US/11/046,456
CURRENT FILING DATE: 2005-01-27
PRIOR APPLICATION NUMBER: US 60/539,605
PRIOR FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 60/619,241
PRIOR FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: US 10/488,423
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: PCT/US02/27746
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-11-046-456-27
Query Match 47.6%; Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.56+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 GLM 4
Db 2 GTM 4
RESULT 2
US-11-046-644-27
Sequence 27, Application US/11046644
Publication No. US20050256036A1
GENERAL INFORMATION:
APPLICANT: Boyle, Bryan

```

; APPLICANT: Funk, Walter
; APPLICANT: Kakitani, Makoto
; APPLICANT: Oshima, Takeshi
; APPLICANT: Park, Emily
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Yagi, Miki
; TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
; FILE REFERENCE: 11926-194001
; CURRENT APPLICATION NUMBER: US/11/046,644
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US 60/539,605
; PRIOR FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/619,241
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-644-27
```

```

Query Match          47.6%; Score 10; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GLM 4
        ||
DB      2 GTM 4
```

```

RESULT 3
US-11-052-168A-38
; Sequence 38, Application US/11052168A
; Publication No. US20050256301A1
; GENERAL INFORMATION:
; APPLICANT: Craik, David James
; APPLICANT: Daly, Noelle Lee
; APPLICANT: Nielsen, Katherine Justine
; APPLICANT: Armishaw, Christopher
; APPLICANT: Clark, Richard James
; APPLICANT: Alewood, Paul Francis
; TITLE OF INVENTION: CYCLISED CONOTOXIN PEPTIDES
; FILE REFERENCE: DAVI-0008
; CURRENT APPLICATION NUMBER: US/11/052,168A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 09/787,082
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: PCT/AU99/00769
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: AU PP 5895
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-052-168A-38
```

```

Query Match          47.6%; Score 10; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 GL 3
        ||
DB      1 GL 2
```

RESULT 4

```

US-11-064-785-1
; Sequence 1, Application US/11064785
; Publication No. US2005025630A1
; GENERAL INFORMATION:
; APPLICANT: PENG, BAIJIAN
; TITLE OF INVENTION: HETEROCYCLIC SELF-IMMOLATIVE LINKERS AND
; FILE REFERENCE: 39766-0143A
; CURRENT APPLICATION NUMBER: US/11/064,785
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 60/547,152
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-064-785-1
```

```

Query Match          38.1%; Score 8; DB 7; Length 4;
Best Local Similarity 33.3%; Pred. No. 1.5e+04;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GLM 4
        |
DB      1 GFL 3
```

```

RESULT 5
US-10-977-367-21
; Sequence 21, Application US/10977367
; Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules That Selectively Home To
; TITLE OF INVENTION: Vasculecture of Premalignant or Malignant Lesions of the
; FILE REFERENCE: 66821-310
; CURRENT APPLICATION NUMBER: US/10/977,367
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/516,118
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-977-367-21
```

```

Query Match          33.3%; Score 7; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 GL 3
        |
DB      3 GV 4
```

```

RESULT 6
US-10-977-367-36
; Sequence 36, Application US/10977367
; Publication No. US20050245445A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules That Selectively Home To
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:02:43 ; Search time 75.3571 Seconds
(without alignments)
29.153 Million cell updates/sec

Title: US-10-805-881-4

Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 990051

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries
1: A_Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	95.5	9	9	ADV56611
2	21	95.5	9	9	ADV57296
3	21	95.5	12	2	AAW64648
4	21	95.5	13	9	ADV57358
5	21	95.5	13	9	ADV56673
6	21	95.5	14	4	AAW97765
7	21	95.5	15	8	ADL14251
8	21	95.5	15	8	ADL14262
9	21	95.5	15	8	ADL14261
10	21	95.5	15	8	ADL14263
11	21	95.5	19	9	ADV57350
12	21	95.5	19	9	ADV56665
13	21	95.5	20	2	AAW64649
14	21	95.5	21	8	ADL14248
15	21	95.5	29	4	AAW14803
16	21	95.5	29	4	ABR33770
17	21	95.5	29	4	AAW27230
18	21	95.5	29	4	ABR28587
19	21	95.5	29	4	ABR19214
20	21	95.5	29	4	AAW65943
21	21	95.5	29	4	AAW54537
22	21	95.5	29	4	ABG48607
23	21	95.5	29	4	AAW02528
24	21	95.5	29	5	ABG36600

25	20	90.9	5	2	AAW33009	AAW33009 Alpha-sub
26	20	90.9	5	2	AAW33008	AAW33008 Alpha-sub
27	20	90.9	5	2	AAW33007	AAW33007 Alpha-sub
28	20	90.9	5	2	AAW33010	AAW33010 Alpha-sub
29	20	90.9	5	2	AAW80134	AAW80134 COOH-term
30	20	90.9	5	2	AAW54549	AAW54549 Cholecyt
31	20	90.9	5	2	AAW54551	AAW54551 Cholecyt
32	20	90.9	5	2	AAW54550	AAW54550 Cholecyt
33	20	90.9	5	2	AAW54548	AAW54548 Cholecyt
34	20	90.9	5	2	AAW41687	AAW41687 Tetrapt
35	20	90.9	5	2	AAW99643	AAW99643 Substance
36	20	90.9	5	2	AAW50325	AAW50325 Neutroph
37	20	90.9	5	2	AAW92660	AAW92660 Human Tac
38	20	90.9	5	3	AAW23028	AAW23028 Mammalian
39	20	90.9	5	3	AAW23025	AAW23025 Human/rat
40	20	90.9	5	3	AAW67576	AAW67576 P antagon
41	20	90.9	5	4	AAW66674	AAW66674 C-term
42	20	90.9	5	4	AAW82430	AAW82430 Fluorinat
43	20	90.9	5	4	AAW82431	AAW82431 Fluorinat
44	20	90.9	5	4	AAW91428	AAW91428 Tachykini
45	20	90.9	5	4	AAW70556	AAW70556 Octopus t

ALIGNMENTS

RESULT 1
ADV56611 standard; peptide; 9 AA.
ADV56611;
ADV56611;
10-MAR-2005 (first entry)
G protein coupled receptor peptide SEQ ID NO 4113.
diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
Unidentified.
WO2004111636-A2.
23-DEC-2004.
17-JUN-2004; 2004WO-EP051158.
17-JUN-2003; 2003EP-00101775.
17-JUN-2003; 2003US-0479061P.
(VIBV-) VIB VZM.
(VIBV-) UNIT GENT.
Kas K, Vandekerckhove J, Kroes J;
WPI; 2005-057893/06.
Identifying a peptide combo which corresponds with a family of proteins,
useful for diagnosing a variety of diseases, drug development or in
agriculture, comprises generating peptides by applying a digest on the
family of protein.
Example; SEQ ID NO 4113; 265PP; English.
The invention relates to a method of identifying a peptide combo which
corresponds with a family of proteins where each of the members of the
peptide combo is derived from a unique protein from the family. The
peptide combo is useful for quantifying specific known splice variants of
one or more particular proteins in a sample, for diagnosing complex
genetic diseases such as cancer, obesity, diabetes, asthma and
inflammation, neuropsychiatric disorders such as depression, for
quantifying one to several hundreds of protein disease markers
simultaneously leading to a more accurate diagnostic sub-classification,

CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating immune levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.

CC Sequence 9 AA:

Query Match 95.5%; Score 21; DB 9; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
 | | | |
 Db 1 FTGLM 5

RESULT 2

ADV57296
 ID ADV57296 standard; peptide; 9 AA.

AC ADV57296;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 4800.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

OS Unidentified.

PN WO2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

PA (VIBV-) VIB VZW.
 (UYGB-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krols L;

PI WPI; 2005-057893/06.

PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.

PS Example; SEQ ID NO 4800; 265pp; English.

CC The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample

CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating immune levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a G-protein coupled receptor peptide
 CC combo.

CC Sequence 9 AA:

Query Match 95.5%; Score 21; DB 9; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXGLM 5
 | | | |
 Db 1 FTGLM 5

RESULT 3

AAM64648
 ID AAM64648 standard; peptide; 12 AA.

AC AAM64648;

DT 23-OCT-1998 (first entry)

DE Synthetic SEB-related peptide (position 13-24).

XX Enterotoxin B; SEB; pyrogenic exotoxin; PERT; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;

KW therapeutic; vaccine; food poisoning.

OS Synthetic.

OS Staphylococcus aureus.

PN WO9829444-A1.

PD 09-JUL-1998.

PF 30-DEC-1997; 97WO-IL000438.

PR 30-DEC-1996; 96IL-00119938.

PA (YISS) YISSUM RES & DEV CO.

PI Kaempfer R, Arad G;

PI WPI; 1998-388042/33.

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s).

PS Example 2; Page 38; 68pp; English.

CC AAM64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PERT), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced by
 CC PERT or by a mixture of PERTs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-
 CC beta genes. The peptides may be used to prepare therapeutics or vaccines
 CC for the treatment of prophylaxis of toxin-mediated activation of T cells
 CC and eliciting protective immunity against toxic shock induced by PERTs.
 CC They can also be used for the treatment of harmful effects (especially
 CC food poisoning) and toxic shock caused by PERT. Antiserum to the peptides
 CC can also be used for alleviating toxic shock induced by PERT

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:18:04 ; Search time 20 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	90.9	10	1	SPRGNK
2	20	90.9	10	2	neurokinin K - pig
3	20	90.9	10	2	neurokinin A - chi
4	20	90.9	10	2	neurokinin II - ye
5	20	90.9	10	2	neurokinin A - ral
6	20	90.9	10	2	neurokinin A - At1
7	20	90.9	10	2	neurokinin A - tw
8	20	90.9	10	2	neurokinin C -
9	20	90.9	10	2	neurokinin B -
10	20	90.9	10	2	neurokinin A-relat
11	20	90.9	10	2	neurokinin I - yel
12	20	90.9	11	1	neurokinin I - s
13	20	90.9	11	1	neurokinin I - s
14	20	90.9	11	1	neurokinin I - s
15	20	90.9	11	1	neurokinin I - s
16	20	90.9	11	1	neurokinin I - s
17	20	90.9	11	2	neurokinin I - s
18	20	90.9	11	2	neurokinin I - s
19	20	90.9	11	2	neurokinin I - s
20	20	90.9	11	2	neurokinin I - s
21	20	90.9	11	2	neurokinin I - s
22	20	90.9	11	2	neurokinin I - s
23	20	90.9	11	2	neurokinin I - s
24	20	90.9	11	2	neurokinin I - s
25	20	90.9	11	2	neurokinin I - s
26	20	90.9	11	2	neurokinin I - s
27	20	90.9	11	2	neurokinin I - s
28	20	90.9	12	2	neurokinin I - s
29	20	90.9	12	2	neurokinin I - s

30	20	90.9	16	2	A60839	neurokinin A homol
31	20	90.9	18	2	B24867	neurokinin II -
32	20	90.9	21	2	JH0361	carassin - goldfis
33	18	81.8	12	2	S07436	neurokinin - afric
34	18	81.8	28	1	LFEBLT	leu operon leader
35	18	81.8	28	1	AG0516	leu operon leader
36	18	81.8	30	2	F95118	hypothetical prote
37	17	77.3	20	2	H49034	nuclear antigen EB
38	17	77.3	28	1	LFEBLT	leu operon leader
39	17	77.3	28	1	G90538	leu operon leader
40	17	77.3	28	2	G85489	leu operon leader
41	16	72.7	16	2	I51879	cystathionine beta
42	16	72.7	22	2	A36399	C-type natriuretic
43	16	72.7	23	2	S43469	heterodisulfide re
44	16	72.7	24	2	S29749	serum albumin - do
45	16	72.7	29	2	S78326	conserved hypothe

ALIGNMENTS

RESULT 1

SPRGNK

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C/Accession: A01560

R/Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.

Biochem. Biophys. Res. Commun. 114, 533-540, 1983

A/Title: Neurokinin K: a novel mammalian tachykinin identified in porcine spinal cord.

A/Reference number: A01560; MUID:83282812; PMID:6576785

A/Accession: A01560

A/Molecule type: protein

A/Residues: 1-10 <KAN>

A/Cross-references: UNIPROT:P01292; UNIPARC:UPI00000312EA

A/Note: The structure of the peptide was confirmed by synthesis

C/Comment: The biological source of this peptide is spinal cord. It stimulates smooth mus

C/Superfamily: neurokinin B precursor

C/Keywords: amidated carboxyl end; hormone; spinal cord

F/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 90.9%; Score 20; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FXGLM 5
| | | |
Db 6 FXGLM 10

RESULT 2

JN0024

C/Species: Gallus gallus (chicken)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: JN0024

R/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A/Reference number: JN0023; MUID:88204263; PMID:2452461

A/Accession: JN0024

A/Molecule type: protein

A/Residues: 1-10 <CON>

A/Cross-references: UNIPROT:P19851; UNIPARC:UPI000003521C

C/Superfamily: substance P precursor

C/Keywords: amidated carboxyl end; neuropeptide; tachykinin

F/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 90.9%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 FXGLM 5

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:17:04 ; Search time 122.5 Seconds
(without alignments)
28.797 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 34439

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprotc_05.80:.*
1: uniprotc_sprot:.*
2: uniprotc_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	13	1	CP1_APLCA
2	20	90.9	10	1	TKN1_SCYCA
3	20	90.9	10	1	TKNB_CHICK
4	20	90.9	10	1	TKNB_GADMO
5	20	90.9	10	1	TKNB_ONCMY
6	20	90.9	10	1	TKNB_RANCA
7	20	90.9	10	1	TKNB_RANRI
8	20	90.9	10	1	TKNC_RANCA
9	20	90.9	10	1	TKNC_PIG
10	20	90.9	10	1	TKNK_RANRI
11	20	90.9	10	1	TKN1_PHYBI
12	20	90.9	10	1	TKS1_AEDAE
13	20	90.9	10	1	TKS2_AEDAE
14	20	90.9	11	1	TKN1_PSEGU
15	20	90.9	11	1	TKN1_PSEGU
16	20	90.9	11	1	TKN1_PSEGU
17	20	90.9	11	1	TKN1_PSEGU
18	20	90.9	11	1	TKN2_PSEGU
19	20	90.9	11	1	TKN3_PSEGU
20	20	90.9	11	1	TKN4_PSEGU
21	20	90.9	11	1	TKN5_PSEGU
22	20	90.9	11	1	TKNA_CAVPO
23	20	90.9	11	1	TKNA_CHICK
24	20	90.9	11	1	TKNA_GADMO
25	20	90.9	11	1	TKNA_HORSE
26	20	90.9	11	1	TKNA_ONCMY
27	20	90.9	11	1	TKNA_RANCA
28	20	90.9	11	1	TKNA_RANRI
29	20	90.9	11	1	TKNA_SCYCA
30	20	90.9	11	1	TKN_ELECT
31	20	90.9	11	1	TKN_ELEM0

32	20	90.9	11	1	TKN1_PHYBI	P08615 phylaalemus
33	20	90.9	11	2	OUAR8_AEDAE	OUAR8 aedes aegypti
34	20	90.9	12	1	TKN1_KASMA	P08613 kassina mac
35	20	90.9	12	1	TKN1_KASSE	P08611 kassina sen
36	20	90.9	14	1	TKNM_RANCA	P40951 rana margar
37	20	90.9	16	1	TKN1_TORNA	Q71248 torpedo mar
38	20	90.9	18	1	TKN2_SCYCA	P08609 scylliorhinu
39	20	90.9	21	1	TKNC_CARAU	P25421 carassius a
40	20	90.9	21	2	Q9PRZ3_ONCMY	Q9PRZ3 oncorhynch
41	20	90.9	21	2	Q9PRZ3_ALIMI	Q9PRZ3 alligator m
42	20	90.9	24	2	Q9PRP3_SPHLE	Q9PRP3 sphyrna lew
43	20	90.9	29	2	Q673E3_9CHLR	Q673E3 dehalococco
44	19	86.4	27	2	Q9XAV0_PORGI	Q9XAV0 porphyromon
45	18	81.8	12	1	TKN2_KASMA	P08614 kassina mac

ALIGNMENTS

```

RESULT 1
CP1_APLCA
ID CP1_APLCA STANDARD; PRT; 13 AA.
AC Q10998;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Cerebral peptide 1 (Cp1)
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyrea; Opisthobranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Ganglion.
RA MEDLINE=97001771; PubMed=844763;
RX Phares G.A., Lloyd P.E.;
RT "Purification, primary structure, and neuronal localization of
RL Peptides 17:753-761(1996).
CC -1- FUNCTION: May function as a peptide transmitter.
CC -1- TISSUE SPECIFICITY: Found predominantly in the cerebral and pedal
ganglia.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Direct protein sequencing.
KM SEQUENCE 13 AA; 1314 MW; 9DBC3CE82C667B05 CRC64;
SQ
Query Match 95.5%; Score 21; DB 1; Length 13;
Best local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FXGLM 5
Db 1 FXGLM 5

```

RESULT 2

```

TKN1_SCYCA
ID TKN1_SCYCA STANDARD; PRT; 10 AA.
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Scylliorhinus canicula (Spotted dogfish) (Spotted catshark).
OS Scylliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carchariniiformes;

```

CC Scyliorhinidae; Scyliorhinus.
OK NCBI_TaxID=7830;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
RN FEBS Lett. 200;111-116(1986).
RN [2]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.";
RN Eur. J. Biochem. 214:469-474(1993).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR: A24867; A24867.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amidaaction; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 10 10 Methionine amide.
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C3AA9 CRC64;

Query Match 90.9%; Score 20; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXGLM 5
|
|
|
|
Db 6 FVGLM 10

RESULT 3
TKNB_CHICK STANDARD; PRT; 10 AA.
ID TKNB_CHICK
AC P19851;
DT 01-FEB-1991 (Rel. 17, Created)
DR 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin L).
OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3] substance P and neurokinin A from chicken small intestine.";
RN Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR: JN0024; JN0024.
DR PDB: 1N6T; NMR; A=1-10.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW 3D-structure; Amidation; Direct protein sequencing; Neuropeptide;
KW Tachykinin.
FT MOD RES 10 10 Methionine amide.
SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5BABI CRC64;

Query Match 90.9%; Score 20; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXGLM 5
|
|
|
|
Db 6 FVGLM 10

RESULT 4
TKNB_GADMO STANDARD; PRT; 10 AA.
ID TKNB_GADMO
AC P69144; P28500;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin L).
OS Gadus morhua (Atlantic cod).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OK NCBI_TaxID=8049;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RN Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR: S23186; S23186.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 10 10 Methionine amide (By similarity).
SQ SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;

Query Match 90.9%; Score 20; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXGLM 5
|
|
|
|

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:06:43 ; Search time 20 Seconds
(Without alignments)
20.669 Million cell updates/sec

Title: US-10-805-881-4

Perfect score: 22

Sequence: 1 FXGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 265581

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/H COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RB COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	90.9	5	1	US-07-753-909B-3 Sequence 3, Appli
2	20	90.9	5	1	US-07-934-553-2 Sequence 2, Appli
3	20	90.9	5	1	US-08-269-288-1 Sequence 1, Appli
4	20	90.9	5	1	US-08-225-474-2 Sequence 2, Appli
5	20	90.9	5	1	US-08-391-910-1 Sequence 1, Appli
6	20	90.9	5	1	US-08-418-994-1 Sequence 1, Appli
7	20	90.9	5	1	US-08-391-814-1 Sequence 1, Appli
8	20	90.9	5	1	US-08-441-591-61 Sequence 61, Appli
9	20	90.9	5	1	US-08-303-362A-61 Sequence 61, Appli
10	20	90.9	5	1	US-08-462-415-1 Sequence 1, Appli
11	20	90.9	5	1	US-08-463-874-1 Sequence 1, Appli
12	20	90.9	5	1	US-08-444-135-1 Sequence 1, Appli
13	20	90.9	5	1	US-08-318-391-1 Sequence 1, Appli
14	20	90.9	5	1	US-07-737-371B-6 Sequence 6, Appli
15	20	90.9	5	2	US-08-257-966-1 Sequence 1, Appli
16	20	90.9	5	2	US-09-265-690C-1 Sequence 1, Appli
17	20	90.9	5	2	US-09-265-690C-4 Sequence 4, Appli
18	20	90.9	5	2	US-08-153-847-1 Sequence 1, Appli
19	20	90.9	5	2	US-09-635-266-4 Sequence 4, Appli
20	20	90.9	5	2	US-10-230-133-4 Sequence 4, Appli
21	20	90.9	5	2	US-09-623-548A-604 Sequence 604, App
22	20	90.9	5	2	US-10-695-536-4 Sequence 4, Appli
23	20	90.9	5	2	US-10-668-565-1 Sequence 1, Appli
24	20	90.9	5	2	US-10-134-187-3 Sequence 3, Appli
25	20	90.9	5	2	US-09-657-276-604 Sequence 604, App
26	20	90.9	5	4	PCM-US95-05600-78 Sequence 78, Appli
27	20	90.9	6	1	US-07-934-553-3 Sequence 3, Appli

28	20	90.9	6	1	US-08-225-474-3 Sequence 3, Appli
29	20	90.9	6	1	US-08-430-238-15 Sequence 15, Appli
30	20	90.9	6	1	US-07-737-371B-5 Sequence 5, Appli
31	20	90.9	6	1	US-07-737-371B-52 Sequence 52, Appli
32	20	90.9	6	2	US-09-317-125-5 Sequence 5, Appli
33	20	90.9	6	2	US-09-428-692-39 Sequence 39, Appli
34	20	90.9	6	2	US-09-428-692-41 Sequence 41, Appli
35	20	90.9	6	2	US-09-623-548A-595 Sequence 595, App
36	20	90.9	6	2	US-09-623-548A-597 Sequence 597, App
37	20	90.9	6	2	US-09-623-548A-601 Sequence 601, App
38	20	90.9	6	2	US-09-657-276-595 Sequence 595, App
39	20	90.9	6	2	US-09-657-276-597 Sequence 597, App
40	20	90.9	6	2	US-09-657-276-601 Sequence 601, App
41	20	90.9	7	1	US-07-712-828B-7 Sequence 7, Appli
42	20	90.9	7	1	US-07-737-371B-8 Sequence 8, Appli
43	20	90.9	7	1	US-07-737-371B-51 Sequence 51, Appli
44	20	90.9	7	2	US-09-428-692-42 Sequence 42, Appli
45	20	90.9	7	2	US-09-623-548A-530 Sequence 530, App

ALIGNMENTS

RESULT 1
US-07-753-909B-3
Sequence 3, Application US/07753909B
Patent No. 5304632
GENERAL INFORMATION:
APPLICANT: Vaudry, Hubert
APPLICANT: Conlon, Michael J.
TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thonnte, Voorhees, and Sease
STREET: 801 Grand, Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,909B
FILING DATE: 19910903
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9106759
FILING DATE: 04-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sease, Edmund J.
REGISTRATION NUMBER: 24,741
TELEPHONE: (515)-288-3667
TELEFAX: (515)-288-1338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Rana ridibunda
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: brain
US-07-753-909B-3
Query Match 90.9%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FXGLM 5
|||||
Db 1 FXGLM 5

RESULT 2
US-07-934-553-2
Sequence 2, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934.553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-2

Query Match 90.9%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FXGLM 5
|||||
Db 1 FXGLM 5

RESULT 3
US-08-269-288-1
Sequence 1, Application US/08269288
Patent No. 5491140
GENERAL INFORMATION:
APPLICANT: Bruns, Robert F.
APPLICANT: Gehlert, Donald R.
APPLICANT: Howbert, James J.
APPLICANT: Lunn, William H.W.
TITLE OF INVENTION: NARPHYL TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46265
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,288
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-1

Query Match 90.9%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FXGLM 5
|||||
Db 1 FXGLM 5

RESULT 4
US-08-225-474-2
Sequence 2, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: IGE Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:13:24 ; Search time 57.5 Seconds
(without alignments)
36.333 Million cell updates/sec

Title: US-10-805-881-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 439079

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	12	US-10-172-425B-16	Sequence 16, Appl
2	21	95.5	15	US-10-525-113-10	Sequence 10, Appl
3	21	95.5	15	US-10-525-113-11	Sequence 11, Appl
4	21	95.5	15	US-10-525-113-12	Sequence 12, Appl
5	21	95.5	15	US-10-525-113-13	Sequence 13, Appl
6	21	95.5	21	US-10-172-425B-17	Sequence 17, Appl
7	21	95.5	21	US-10-525-113-2	Sequence 2, Appl
8	21	95.5	29	US-09-864-761-34512	Sequence 34512, A
9	20	90.9	5	US-09-265-690C-1	Sequence 1, Appl
10	20	90.9	5	US-09-265-690C-4	Sequence 4, Appl
11	20	90.9	5	US-10-230-133-4	Sequence 4, Appl
12	20	90.9	5	US-10-053-669-1	Sequence 1, Appl
13	20	90.9	5	US-10-053-669-4	Sequence 4, Appl
14	20	90.9	5	US-10-134-187-3	Sequence 3, Appl
15	20	90.9	5	US-10-688-741-3	Sequence 3, Appl
16	20	90.9	5	US-10-695-536-4	Sequence 4, Appl
17	20	90.9	5	US-10-805-881-1	Sequence 1, Appl
18	20	90.9	5	US-10-805-881-4	Sequence 4, Appl
19	20	90.9	5	US-10-720-039-3	Sequence 3, Appl
20	20	90.9	5	US-10-497-628-15	Sequence 15, Appl
21	20	90.9	5	US-10-451-304-12	Sequence 12, Appl
22	20	90.9	5	US-11-018-690-4	Sequence 4, Appl
23	20	90.9	5	US-11-066-697-604	Sequence 604, App
24	20	90.9	5	US-11-025-494-3	Sequence 3, Appl
25	20	90.9	6	US-10-168-789A-38	Sequence 38, Appl
26	20	90.9	6	US-10-497-628-14	Sequence 14, Appl
27	20	90.9	6	US-11-066-697-595	Sequence 595, App

28	20	90.9	6	US-11-066-697-597	Sequence 597, App
29	20	90.9	6	US-11-066-697-601	Sequence 601, App
30	20	90.9	7	US-10-036-542-110	Sequence 110, App
31	20	90.9	7	US-10-036-542-111	Sequence 111, App
32	20	90.9	7	US-10-168-789A-37	Sequence 37, Appl
33	20	90.9	7	US-10-134-187-2	Sequence 2, Appl
34	20	90.9	7	US-10-688-741-2	Sequence 2, Appl
35	20	90.9	7	US-10-720-039-2	Sequence 2, Appl
36	20	90.9	7	US-10-497-628-13	Sequence 13, Appl
37	20	90.9	7	US-11-066-697-530	Sequence 530, App
38	20	90.9	7	US-11-066-697-596	Sequence 596, App
39	20	90.9	7	US-11-066-697-607	Sequence 607, App
40	20	90.9	7	US-11-025-494-2	Sequence 2, Appl
41	20	90.9	8	US-09-910-552-36	Sequence 36, Appl
42	20	90.9	8	US-10-168-789A-36	Sequence 36, Appl
43	20	90.9	8	US-10-643-465-36	Sequence 36, Appl
44	20	90.9	8	US-10-497-628-12	Sequence 12, Appl
45	20	90.9	8	US-11-066-697-583	Sequence 583, App

ALIGNMENTS

RESULT 1
US-10-172-425B-16
; Sequence 16, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Axrad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172.425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150.947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-172-425B-16

Query Match 95.5%: Score 21; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0;

Qy 1 FXGLM 5
Db S FTGLM 9

RESULT 2
US-10-525-113-10
; Sequence 10, Application US/10525113
; Publication No. US2005024009A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: CARER, Francis J.
; APPLICANT: BAKER, Matthew
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
; TITLE OF INVENTION: ENTEROTOXIN B
; FILE REFERENCE: MER-138
; CURRENT APPLICATION NUMBER: US/10/525.113
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009116

```
/ PRIOR FILING DATE: 2003-08-18
/ PRIOR APPLICATION NUMBER: EP 02018229.1
/ PRIOR FILING DATE: 2002-08-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 10
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-525-113-10
```

```
Query Match          95.5%; Score 21; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 FXGLM 5
        | |||
Db      11 FTGLM 15
```

```
RESULT 3
US-10-525-113-11
/ Sequence 11, Application US/10525113
/ Publication No. US20050240009A1
/ GENERAL INFORMATION:
/ APPLICANT: MERCK PATENT GMBH
/ APPLICANT: CARR, Francis J.
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARTER, Graham
/ TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
/ FILE OF INVENTION: ENTEROTOXIN B
/ FILE REFERENCE: MER-138
/ CURRENT APPLICATION NUMBER: US/10/525,113
/ PRIOR FILING DATE: 2005-02-18
/ PRIOR APPLICATION NUMBER: PCT/EP2003/009116
/ PRIOR FILING DATE: 2003-08-18
/ PRIOR APPLICATION NUMBER: EP 02018229.1
/ PRIOR FILING DATE: 2002-08-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 11
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-525-113-11
```

```
Query Match          95.5%; Score 21; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 FXGLM 5
        | |||
Db      8 FTGLM 12
```

```
RESULT 4
US-10-525-113-12
/ Sequence 12, Application US/10525113
/ Publication No. US20050240009A1
/ GENERAL INFORMATION:
/ APPLICANT: MERCK PATENT GMBH
/ APPLICANT: CARR, Francis J.
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARTER, Graham
/ TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
/ FILE OF INVENTION: ENTEROTOXIN B
/ FILE REFERENCE: MER-138
/ CURRENT APPLICATION NUMBER: US/10/525,113
/ PRIOR FILING DATE: 2005-02-18
/ PRIOR APPLICATION NUMBER: PCT/EP2003/009116
/ PRIOR FILING DATE: 2003-08-18
/ PRIOR APPLICATION NUMBER: EP 02018229.1
/ PRIOR FILING DATE: 2002-08-21
```

```
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 12
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-525-113-12
```

```
Query Match          95.5%; Score 21; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 FXGLM 5
        | |||
Db      5 FTGLM 9
```

```
RESULT 5
US-10-525-113-13
/ Sequence 13, Application US/10525113
/ Publication No. US20050240009A1
/ GENERAL INFORMATION:
/ APPLICANT: MERCK PATENT GMBH
/ APPLICANT: CARR, Francis J.
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARTER, Graham
/ TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
/ FILE OF INVENTION: ENTEROTOXIN B
/ FILE REFERENCE: MER-138
/ CURRENT APPLICATION NUMBER: US/10/525,113
/ PRIOR FILING DATE: 2005-02-18
/ PRIOR APPLICATION NUMBER: PCT/EP2003/009116
/ PRIOR FILING DATE: 2003-08-18
/ PRIOR APPLICATION NUMBER: EP 02018229.1
/ PRIOR FILING DATE: 2002-08-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 13
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-10-525-113-13
```

```
Query Match          95.5%; Score 21; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 FXGLM 5
        | |||
Db      2 FTGLM 6
```

```
RESULT 6
US-10-172-425B-17
/ Sequence 17, Application US/10172425B
/ Publication No. US20030147908A1
/ GENERAL INFORMATION:
/ APPLICANT: Kaempfer, Raymond
/ APPLICANT: Arad, Gila
/ TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
/ FILE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
/ FILE REFERENCE: A31967-PCT-USA-A 066031.0164
/ CURRENT APPLICATION NUMBER: US/10/172,425B
/ PRIOR FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: 09/150,947
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: PCT/IL97/00438
/ PRIOR FILING DATE: 1997-12-30
/ PRIOR APPLICATION NUMBER: ISRAEL 119938
/ PRIOR FILING DATE: 1996-12-30
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 17
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 03:09:53 ; Search time 3.57143 Seconds
(without alignments)
4.243 Million cell updates/sec

Title: US-10-805-881-4

Sequence: 1 FXGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues
Total number of hits satisfying chosen parameters: 7285

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	72.7	28	7	US-11-021-441-50
2	15	68.2	8	7	US-11-054-515-3132
3	15	68.2	12	1	US-10-923-605-4
4	15	68.2	12	1	US-10-934-818-4
5	15	68.2	13	1	US-10-511-559-478
6	15	68.2	13	1	US-10-511-559-479
7	15	68.2	13	1	US-10-511-559-480
8	15	68.2	13	1	US-10-511-559-481
9	15	68.2	13	1	US-10-511-559-482
10	15	68.2	16	7	US-11-054-515-2157
11	15	68.2	19	1	US-10-503-575-149
12	15	68.2	24	1	US-10-503-575-161
13	15	68.2	24	1	US-10-989-226-31
14	15	68.2	30	1	US-10-966-501-177
15	14	63.6	20	7	US-11-022-562-147
16	14	63.6	21	1	US-10-939-890-523
17	14	63.6	21	1	US-10-939-890-523
18	14	63.6	21	1	US-10-939-890-551
19	14	63.6	21	1	US-10-939-890-552
20	13	59.1	8	7	US-11-054-515-3098
21	13	59.1	10	1	US-10-614-589-45
22	13	59.1	11	1	US-10-614-589-47
23	13	59.1	12	7	US-11-016-706-49
24	13	59.1	12	7	US-11-054-515-2884
25	13	59.1	14	7	US-11-054-515-2374

26	13	59.1	17	1	US-10-723-207-63	Sequence 63, Appl
27	13	59.1	17	7	US-11-054-515-3025	Sequence 3025, Ap
28	13	59.1	18	7	US-11-054-515-2752	Sequence 2752, Ap
29	13	59.1	18	7	US-11-054-515-2802	Sequence 2802, Ap
30	13	59.1	18	7	US-11-054-515-2880	Sequence 2880, Ap
31	13	59.1	18	7	US-11-054-515-2917	Sequence 2917, Ap
32	13	59.1	20	7	US-11-022-562-175	Sequence 175, App
33	13	59.1	20	7	US-11-022-562-176	Sequence 176, App
34	13	59.1	20	7	US-11-054-515-1131	Sequence 2131, Ap
35	13	59.1	21	1	US-10-939-890-597	Sequence 597, App
36	13	54.5	7	1	US-10-516-768-35	Sequence 35, App
37	12	54.5	9	7	US-11-032-498-7	Sequence 17, Appl
38	12	54.5	9	7	US-11-032-498-17	Sequence 17, Appl
39	12	54.5	9	7	US-11-054-515-3200	Sequence 3200, Ap
40	12	54.5	10	7	US-10-502-145-34	Sequence 25, Appl
41	12	54.5	11	1	US-10-502-145-34	Sequence 34, Appl
42	12	54.5	13	1	US-10-939-890-192	Sequence 192, App
43	12	54.5	13	1	US-10-511-559-113	Sequence 113, App
44	12	54.5	13	1	US-10-511-559-114	Sequence 114, App
45	12	54.5	13	1	US-10-511-559-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-11-021-441-50
Sequence 50, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A.
APPLICANT: LUCKERT, William S., Jr.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA,
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 28
TYPE: PRT
ORGANISM: Bacillus anthracis
US-11-021-441-50
Query Match 72.7%; Score 16; DB 7; Length 28;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 3; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
Gy 1 FXGL 4
Db 17 FSGI 20
RESULT 2
US-11-054-515-3132
Sequence 3132, Application US/11054515
Publication No. US20050255532A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23p3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3132
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-054-515-3132

Query Match          68.2%; Score 15; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1,5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GLM 5
      |||
Db      4 GLM 6

RESULT 3
US-10-923-605-4
/ Sequence 4, Application US/10923605
/ Publication No. US20050249727A1
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ APPLICANT: Neuralab Limited
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 152703-004740US
/ CURRENT APPLICATION NUMBER: US/10/923,605
/ CURRENT FILING DATE: 2004-08-20
/ PRIOR APPLICATION NUMBER: US/09/322,289
/ PRIOR FILING DATE: 1999-05-28
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Abeta33-42
/ OTHER INFORMATION: peptide with carboxyl terminal Cys residue
/ OTHER INFORMATION: inserted
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (2)_
/ OTHER INFORMATION: Xaa = amino heptanoic acid
US-10-923-605-4

Query Match          68.2%; Score 15; DB 1; Length 12;
```

```
Best Local Similarity 100.0%; Pred. No. 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GLM 5
      |||
Db      3 GLM 5

RESULT 4
US-10-934-818-4
/ Sequence 4, Application US/10934818
/ Publication No. US20050255122A1
/ GENERAL INFORMATION:
/ APPLICANT: Schenk, Dale B.
/ APPLICANT: Neuralab Limited
/ TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
/ FILE REFERENCE: 152703-472000US
/ CURRENT APPLICATION NUMBER: US/10/934,818
/ CURRENT FILING DATE: 2004-09-02
/ PRIOR APPLICATION NUMBER: US 60/067,740
/ PRIOR FILING DATE: 1997-12-02
/ PRIOR APPLICATION NUMBER: US 60/080,970
/ PRIOR FILING DATE: 1998-04-07
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Abeta33-42
/ OTHER INFORMATION: peptide with carboxyl terminal Cys residue
/ OTHER INFORMATION: inserted
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (2)_
/ OTHER INFORMATION: Xaa = amino heptanoic acid
US-10-934-818-4

Query Match          68.2%; Score 15; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GLM 5
      |||
Db      3 GLM 5

RESULT 5
US-10-511-559-478
/ Sequence 478, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 478
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

THIS PAGE BLANK (USPTO)